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ALOSO283 Homo sapi
AX081143 Sequence
AY008763 Homo sapi
ALB34294 Homo sapi
ARF199403 Homo sapi
ARF194031 Homo sapi
ARV008764 Mus muscu
AC126239 Felis cat
AC126239 Felis cat
AC126239 Felis cat
AC126239 Homo sapi
AC0092294 Rattus no
AB060822 Macaca fa
BC008589 Homo sapi
AB07405 Homo sapi
AB07405 Homo sapi
AC127470 Pan trogl
AC126377 Canis fam
AC098923 Rattus no
AC209823 Rattus no
AC209923 Rattus no
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-O=/Cgn2_1/USFTO_spool/US09848852/runat_16122002_132040_19132/app_query.fasta_1.519
-OB-GenEmbl -QFWT=fastap -SUFFTX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UOTALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MINO -ALIGN=15 -MODE-LOCAL
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-USER-US0848852_eCGN_1_1 3637_etunat_16122002_132040_19132 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MANP -LARGEQUERY -NGG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THERBADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                    December 16, 2002, 20:17:55 ; Search time 3156 Seconds (without alignments) 3061.512 Million cell updates/sec
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              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                        - nucleic search, using frame_plus_p2n model
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Martinsried, GERNANY,

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DRF2); Emails, wiemannédkíz-heidelberg.de;
Research Center (DRF2); Emails, wiemannédkíz-heidelberg.de;
Sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing
consortium of the German Genome Project.

This clone (DRF2P586KO919) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Purther
information about the clone and the sequencing project is available
at http://www.m.ps.biochem.mpg.de/proj/cDNA/.

Location/Qualifiers
irce // Organism="Homo sapiens"
// Ab_xref="taxon:9606"
// Clone="DRE2P586KO919"
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VHFPNSFFYDKLRTKGYDGYKRWTKNYDIFNKELLIPIHLEVHWSLISVDVRRRTIT
FYSDRTLINTRCPKHIAKYLQAEAVKKDRLDFHQGWGYFKMNVARQNNDSDCGAFVL
QYCKHLALSQPFSFTQQDMFKLRRQIYKELCHCKLIV"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
Direct Submission
Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
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/protein_id="CAB43384.1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2206)
Gong, L. and Yeh, E.T.
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Board of Regents, The University of
Location/Qualifiers
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a 612 c 605 g 49E
Sequence 9 from Patent W00109292.
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                              AX081143.1 GI:13170039
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Best Local Similarity:
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            DEFINITION
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Gong, L. and Yeh, E.T.
Direct Submission
Submitted (04-OCT-2000) Institute of Molecular Medicine, University
of Texas-Houston, 2121 W. Holcombe Blvd. 928, Houston, TX 77030,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY008763 2224 bp mRNA linear PRI 21-NOV-2000
Homo sapiens sentrin/SUMO-specific protease (SENP3) mRNA, complete
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yeh, E.T., Gong, L. and Kamitani, T.
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1. .2224
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Conservative:
Mismatches:
Indels:
                                                           Length:
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                                                          1.09e-164
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Best Local Similarity:
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Shimbara, N., Jeon, Y.J., Kim, K.I., Nishimori, S., Suzuki, T., Uchida, S., Shimbara, N., Tanaka, K. and Chung, C.H.

Direct Submission

Submitted (28-OGT-1999) Molecular Biology, Seoul National University, Shillin-dong san 56-1, Seoul 151-742, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF199459 2258 bp mRNA linear PRI 31-OCT-2001
Homo sapiens SUMO-1 specific protease 3 (SSP3) mRNA, complete cds.
AF199459
1617 TGTGGCCAGGCAGAGATAATGACAGTGACTGTGGTTGCTTTGTATTGTACTGCAAGCA 1676
                                                                                                                                                         1677 TCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGACATGCCCAAACTTCGTCGGCA 1736
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Matches:
Conservative:
Mismatches:
Indels:
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German

Cancer

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LAHPKNHLSPQGGGATPQVPSPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSG
PPWEEDGLEWTPKSPLDPDSGLLGCTPLPNGFGGQSGPEGERGLAPPDASILISRVCSI
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FNRELLLIPHLEVHWSLISYDVRRRTTYYPDSQRTLMRRCFKHIAKTLQABANKRDR
LDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKE
                                                                                    This clone (DKFZp762A152) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                    /tissue_type="melanoma (MeWo cell line)"
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DH10B; sites NotI + SalI"
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               Clone from S. Wiemann, Molecular Genome Analysis, German Cance
Research Genter (DKF2); Email s. WiemanneGMffz-heitelberg-de;
Sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the
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   Submitted (09-JUL-2002) 1, D-85764 Neuherberg,
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Conservative:
Mismatches:
Indels:
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                                                                                                    pGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValValGluLy 100
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom.
1 (bases 1 to 2269)
Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSM805332 2269 bp mRNA Homo sapiens mRNA; cDNA DKFZp762A152 (from
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (Dases 1 to 1707)

Nishida, T., Tanaka, H. and Yasuda, H.

A novel mammalian Smt3-specific isopeptidase 1 (SMT3IP1) localized in the nucleolus at interphase

Eur. J. Blochem. 267 (21), 6423-6427 (2000)
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                                                                                         nLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArgValAl
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                                                                                                                                                                                                                                                                                                                     pSerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTyrLeuGlnAlaGl
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Mus musculus SMT3 isopeptidase 1
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GLRWTPKSPLDPDSGLLSCTLPNGFGGLSGPEGERSLAPPDASILISWCSIGDHVAQ
ELPOSSDLGJAEEAARGTGEKAGQHSPLREBHVTCVQSILDEFLQTYGSLIPLSTDEVV
EKLEDIFQQESTPSRKSLVLQLIOSYQRMSGNARGKRSYGNGKRHYLTMDDLGTLYG
QNWLNDQWNNWTGDLVMDTVPEKVUFFVBFRTYGYGNGCWRWTRNVDIFNKELL
LIPHHLEVNWSLISWDWRRFTITYFDSGRTLARRCRHIAKTAGARAWKRDRLDFHQG
WKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMFKLRRQIYKELCHCKL
                                 of
                                   Tokyo University
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Nishida,T., Tanaka,H. and Yasuda,H.
Direct Submission
Submitted (13-OCT-1999) School of Life Science, Tokyo Universi
Pharmacy and Life Science, 1432-1 Horinouchi, Hachioji, Tokyo
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Matches:
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1. 1707
Corganism="Mus musculus"
/db_xref="taxon:10090"
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Query Match:
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2 (bases 1 to 2174)
Gong,L. and Yeh,E.T.
Direct Submission
Submitted (04-007-2000) Institute of Molecular Medicine, University
of Texas-Houston, 2121 W. Holcombe Blvd. 928, Houston, TX 77030,
                                                                                                                                                                                                                                                                                                                                                                                                 AY008764 2174 bp mRNA linear ROD 21-NOV-2000 Mus musculus sentrin/SUMO-specific protease (SENP3) mRNA, complete
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                         lHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyrAspGlyValLy
                                                                                  sArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuIleProIleHisLe
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Yeh, E. T., Gong, L. and Kamitani, T.
Ubiquitin-like proteins: new wines:
20267842
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1. 2174
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="11"
1. .2774
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52. .1758
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/db_xref="G1:11245813"

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ONWLNDQVMNMYGDLVWDTYPEKVHFRYSFRRHYGYGBLYRRKELL
LIPIHLEVHWSLISYDVRRRTITYFDSQRTLRRRCFKHIAKYLQABAVKKDRLDFHQG
WRGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSTQQDMPKLRRQIYKELCHCKL
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        MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHis-LeuAl

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                                                                                                                                                                                                                                                                                                                                                                                  n \\ \texttt{GluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLy}
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1 (bases 1 to 139405)

Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjami, B., Blakseley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Lee-Lin, S.-Q., Legaspli, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pagulirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Tuchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Shang, L.-H., and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC126239 139405 bp DNA linear HTG 04-JUL-2002 Felis catus clone RP86-474H17, WORKING DRAFT SEQUENCE, 12 unordered
                     1659 CCTGGCCCTGTCTCAGCCATTCAGCTTCAGCCAGGAGACATGCCCAAACTCCGTCGTCGTA 1718
240 pSerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTyrLeuGlnAlaGl 260
                                                                                  uAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAs 280
                                                                                                                                                                                                                                               sLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgArgGl 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 7.22x in Q20 bases; agarose-fp Quality coverage: 6.57x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                           Web site: http://www.nisc.nih.gov
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Center clone name: 474H17
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HTG; HTGS_PHASE1; HTGS_DRAFT
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                               2527: contig of 2527 bp in length 2627: gap of unknown length 5397: gap of unknown length 5397: gap of unknown length 7601: contig of 2204 bp in length 7701: gap of unknown length 7701: gap of unknown length 10008: gap of unknown length 12523: contig of 2515 bp in length 16521: contig of 2515 bp in length 16521: contig of 2515 bp in length 16521: contig of 3598 bp in length 16521: contig of 3598 bp in length 24505: contig of 8184 bp in length 24505: contig of 11336 bp in length 3641: gap of unknown length 3641: contig of 11408 bp in length 47549: contig of 11408 bp in length 66243: contig of 18694 bp in length 101568: gap of unknown length 66243: contig of unknown length 101568: contig of unknown length 101568: contig of 34925 bp in length 101568: gap of unknown length 101568: contig of 38037 bp in length
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66344. .101268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Felis catus"
/db_xref="taxon:9685"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.07e-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .139405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            969.50
22.51%
22.30%
54.71%
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οy	1	MetryrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHis-LeuA	
Dp	29569	:::	
Oy Dp	20	aProProAspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGl 40 	
Qy Db	40	nGluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLy 60 	
ΟY	9	salaGlyGlnHisSerProLeuArgGluGluHisValThrCysVal 75	
Ω	29749	92299	
οy	75	15	
qq	29809	CCAGACGGCCGGCCCTTCTCTCTCTCAGCTCCTAAGTTGGAGTGTGGAGGCCTCA 29868	
δy G	76		
δλ	ω	rLeulleProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGlnGl 108	
QQ	29928	CTCATTCCCCTCAGCACTGATGAGGTGGTGGAGAAACTGGAGGACATCTTCAGCAGGA 29987	
δý	108	uPheSerThrProSer 113	
qq	29988	GTTCTCT	
δλ	113	113	
g	30048	CTGAGGGGCCCCTAGGGGTCAGGGGTCGGGAGAGATGCTGCCCCAGAGGGACCGACGCAGG 30107	
ογ	113	113	
Д	30108	GGAGGAGGAGGAGCAGGGACCGAGGGGAGGAATCTGCAGGTGAAGCGCGAAGCCCCTG 30167	
δy	113	113	
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δy	113	113	
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οy	114	122	
qq	30348	TCGTCTCTTGTGTGACTCCACCCTTGGCCTACTCAGGAGGGCCTGGTGCTG	
Qy Db	122	eGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArgValAlaTyrIy 142 	
ΟŽ	142	sArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnA	
QQ	30468		
οy	162	pGlnVal 164	
QQ	30528	-0	
οy	164	164	
οg	30587	GGCCCTCTGCTCGGGGAGCCCTGTGCCCATGCTGCGCCCTCCATGGCAAGTTGCCGCCC 30646	
δλ	165		

g	30647		30706
ò	179	e Λ σ	180
S 2	1 6		U
Q C	30/07	GGT = AGGCCTGACAGGGTACTTCAGTCCCCAGGAGAACTTCTGCAGATCCCAGCAGTTT	30/05
δy	180		180
οg	30766	TGCACTCCCTTTGATCTCTTCCCTTTTCATGGAGGGAGGATCTTTGTTTG	30825
Q	180		180
QΩ	30826	GGTAAAAGGCGGTCTGTTAAATTCAAACCTGTAACCTAGGTCCTGAACTTCTCTGTGTTCCT	30885
Οy	180		180
qq	30886	TTCCCCCCCAGTCGGCAGTGGTTCTCCCTGTGGCTCACCCCACCAGTTGGGAGGGGCAGCA	30945
Qy	180		180
Dp	30946	GGAAGAGAATTGGGTTTCTGCCCCCAGTGGATTGCAGTGGAGGTTGTTGAAACTGGCCCT	31005
Qy	180		180
οgα	31006	TGGAGCCCCAGTGACATGGAGCGGACTGGGCGGAGGAGCTTGGCAGGGAGGCCTGAAGC	31065
ò	181	HisPhepheAsnSerPh	186
qq	31066	TCTTTTAACTCCATCCAGCTCTTTTGTGTCATTGGCACAGGTGCATTTCTTCAACAGTTT	31125
δy	186	ePheTyrAspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsn	205
qq	31126	CTTCTACGATAAACTCCGTACCAAGGTTATGATGGGGTGAAAAGGTGGACCAAAAAGGT	31185
δý	205		205
qq	31186	GAGTTGCCAGTTCACGTGTATGTGGGTAACGCCTTGCCTGTAAAGGATTAGAGTTCCGCT	31245
Qy	205		205
qq	31246	TTCTAGGAGTCCCTTCCCTGAGGCTGCTCACTCAGTTCTAGTAACATGGGTCTTCTG	31305
QY	205		205
QQ	31306	TGTGTTCGGTACTGTCGTGGGCAGCAAGGACTCGGTGTTAAGTAAG	31365
Qy	205		205
qq	31366	TTCGTGGAGTGTGAATAAGTAAAGTTAAATTTCAGCTAGCGTTAGGCGCCGTGAACAAATT	31425
Qy	205		205
qq	31426	AAAAGGGAGATGTAGTAGCGTGGAATGTGGGTGGCTCCGGGAAGGCCACTCTTCTCTGAG	31485
Qγ	205		205
Db	31486	CCTGGAATGACGAGGGCCCGGTCACGTGTGGCTCGGGGGCAAGAGTGGTTTAAGGCGAAGG	31545
δy	205		205
qq	31546	GGACGGCGAGTACGTGGGACACAAGGTGAGACTGGGGGGGG	31605
Οy	205		205
QQ	31606	TGTCTGGTGGTGGGGCAGGGTGAGCGGGGGGAATATGATCAGAAGCTTGGCCAGGGC	31665
Qy	205		205
qq	31666	TGATCGCGTGGGGCGTGGAGGCCGCCGTCACCGTGTGCGCTGAGGCGCCCGTTGACGAGCC	31725
Qγ	205		205

31785 Qy 245 uAsnArgArgCysProLys	5   00 32866	uc		32925 AATCCAGTGGCGGCACTCGAGGCGGAAGGGTGGGCCTGGGGCCTCTGAGGAGCAAACCTG	205 Qy 251 251	Db 32985 GGCTTGGTGCCTGTGACCACCATACCCCGGGCTCCTGTGGGAGACACCGGGCATCGCTCC 33044	Qy 252	CTCCTTTTCTCCGTCTGCACAGCATATTGCCAAGTACCTACAGGCAGAGGCCGTGAAGAA 33	Oy 264 sAspArgLeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMet 279	Db 33105 AGACCGGCTGGATTTCCACCAGGCTGGAAAGGTTACTTCAAAATGGTAAGTTTCTAGAG 33	279	33165 GGAGGAGTACGGGGTGGTGACAGAGGTAAGGCAGGAGGCCAGAAGTTGAGGCCACACCCCT 33	280AsnValAlaakrgGlnAs	33225 AGGAGCCTCCAAACGAAGGGCCTGCCTTCTCTTCTTGGAATGTGGCCAGGCAGAA	285 nAsnAspSerAspCysGlyAlaPheValLeu	33285 TAATGACAGTGACTGCGGTGCCTTTGTGTTACAGGTAAGCAGATGGCAGCTGGGTTAAAG	29	Db 33345 GGCTGGGCAGGAGGAGGCAGGCTGTTCTGCAACCCGCCCCGCCCCGTTGCTCACAGCCC 33404	Qy 295 295	Db 33405 CTTGTGGAGCAGAGTAACCTTAGGTGTCAGAAAGGGCAAACATGGATTTCGTCGGCTC 33464	Qy 295 295	Db 33465 TCCTGGCTTCCCCGTCCCACATCGGGACTGGGTCTCTTGCTTCTTGGTTTCTGGCCCTAA 33524	Qy 295 295	Db 33525 GAAGAGTGGCCTCCTAACCGCCAATGCAGAGTATTTAACACCGGGTATTTCAGGTACCA 33584	Qy 295 295	Db 33585 AGAGCAGGATTTTAGACTTTGAGCCCCAGGCTGGGGCACCTTGGCTCCCTTTGTGAAAT 33644	QY 295 295	Db 33645 GTGGATGTTCTCTGAAAGTTCCAGGGAGGTGGATCTCACTCA	Qy 296GlnTyrCysL	5 Db 33705	Qy 299 ysHisLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgA	. Db 33765	0 10	Oy 319 rgGlnIleTyrLysGluLeuCysHisCysLysLeuThrVal 332 	Oy 264  Oy 279  Oy 279  Oy 280  Oy 280  Oy 285  Oy 285  Oy 285  Oy 295  Oy 296
205		Db 31786 AGCAGGGGACTAACTAGGAGGCGAGCAAAGGAGGCGAGACAGAC	Qy 205 2	Db 31846 TGAGGGAGGAGGAGGGCTCTCTAGGATGGGTTTTGCAGGTAGAACCGAAGTACTTTC 3	Oy 205	31906 TGGAGGGTTGGACGAGGGAATGAAGAAAACTCGGAATCAGGGTGATGCCTGGGTTTGTA		Db 31966 GCAGACGTTACTGGGGAAGATAGGAGAGCACTTTTGGCGAGGGGGAAAAGATAGTTCT 3	205	32026 CGTTAGTTTCCCTGCCTGCAATTCCAAGGCCAGGAAATTTCTACAGTGAGGTAGGACCG	205	32086 TGGGCTGCAGCATTTCTTAGTTTCTGTCCCCAGGCTCAGGAGCTCACACCCTCCCGACC	205	32146 TGGCAGGCCTGCTCCCGATAGAGGTGGGGGGACCTACAGTGAAAGAACTTGGCCTCTGCA	205	32206 TACTGCATCTGAGTCCCACCTCTGCCCTTCCGTGACCTTCAGCAAGTTGCCTAGTCTTC	205	32266 TAAGCTGCCGTTTCCTCCGTTAGATCGAGGGAGGGAACTTCCTCGGAGGATTGTTGTTGTG	205	32326 AACTGACCGACCAGTTGCCGGGGACCCAGCGTTGTCCTCGGTGTGACTTAATTCTCAGAA	205	32386 CAAACAGAGGTAGCGGCTGTCGTTTCCAGTGAAGAGAAGGGGGGGTATAGAGTGG	205	32446 TOGOCCATGGCCACGAGCTAGGAAAGGCAGGAGCTACATCTAAAACCCCCAGTTAGATCTAAAACCTAGATCTAAAAAAAA	30 C	32506 CCAGAGAGCTGAGCCTCGGTTCTTCGCTCCTGAGCACTGGTACCTTTAAAAGGAAAAG	205	32566 TACCCGGGCCATCCTGGGCTCTCAGGTGTGTGTCTGACACACGCCCTTTCCGGTGAGGG	205	32626 CIGGGCCTIGTACCTCCCATGCGGCTTCCTGCCAGCGCCTCCACTCGTCTAAAACCC	205	32686 TCGTGACGGTAGGCGGGACTCTCGTGCCCTGACCAGACCCCTGGCACTGCCCCTTTA		206 -ValAspilePheAsnLysGluLeuLeuLeulleProileHisLeuGluValHisTrpSe	205 CGTTAGTTTCCCTGCCCTGCAATTCCAAGGCCAGGAAATTTCTACAGGGGCCG 205 CGTTAGTTTCCTGCCCTGCCAATTCCAAGGCCAGGAAATTTCTACAGGGGCCC 205 CGTTAGTTTCCTGCCCTGCAATTCCAAGGCCAGGAAATTTCTACAGGGGCCC 205 CGTTAGTTTCCTGCCCTTGCCCCTGCCCTCAGGAAGTTCTTGCA 205 CGTTAGTTTCCTGCCCTTGCCCCTTCCGTGAAAGTTCTTGCA 205 CGTTAGTTTCCTGCCCTTGCCCCTTCCGTGAAAGTTCTTGCA 205 CGTTAGTTTCCTCCCGGGGACCCTCGGGGAGGATTGTTGCA 205 CGTTAGTTTCCTCCCGTTAGATCGAGGGAGGAACTTCCTCGGAAGTTGTTGCA 206 CGAAGCTGCCGTTTCCTCCGGTTAGATCGAGGGAGGAACTTCCTCGGAAGTTGTTGCTGC 207 CGAAGTGCCCGTTTGCCGGGGACCCTGGGAGGAACTTCCTCGGAAGATTGTTGTGGA 208 CGAAACTGCCCACTTGCCGGGACCCAGGGAGGAACTTCCTCGGAGGATTGTTGTGGC 209 CGAAGTGCCCACTTGCCGGGACCCTTCCAGTGAAAGGCCGAGGATTGTTGTTGGCT 201 CGAAGTGCCCACTGCGGTTCCTTCAGTTCCAGTGAAAGGCCGCCCTTTAATTCTCAGAAG 202 CGAAGTGCTCAGGAAAGGCAGGAGCCCTCTGAGAGGG 203 CGAAGTGCTCTCAGGTTCTCTCAGTGCTCTTAAATCTCTTAAATGTTTTAATTCTCAGAAGCCCCCCTTCCGGTGGAGGG 205 CGAAGTGCTCTCAGGTTCTCCTCTCAGGTGCTCTTAAATGTTTTAATTCTCTAGAAGG 206 CGAAGTGCTCTCAGGTTCTCTCCTCTCAGGCCCCCTTCCGGTGGAGGG 207 CGCCCATGGCCTTCTCAGGTTCTCTCTCTCTCTCTCTCTC

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87318 TIGTACTCTTCCCAATGGCTTTGGGGGACCACCCGGCCAGAAGGGGAACGAGATCGCTGGC 87259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHis-LeuAl 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87258 ACCCCCTGATGCCACCATCCTCATCAGCAACGTGTGTAGCATCGGGGACCATGTGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 aProProAspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGl
            8780 78984: contig of 10205 bp in length 9885 79084: gap of unknown length 9085 93446: contig of 14362 bp in length 91847 93546: gap of unknown length 102175: contig of 8629 bp in length 102275: gap of unknown length 102275: gap of unknown length 11868: contig of 29410 bp in length 1186 131785: gap of unknown length 1186 131785: gap of unknown length 1186 12128: contig of 29643 bp in length. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1406 others
  unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
                                                                                                                                                                                                                         /organism="canis familiaris"
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/clone="RP81-332E11"
/clone_lib="RP81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
131786. 161428
/note="assembly_fragment"
41863 c 41233 g 37340 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
4835. .7325
/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93547. .102175
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:right"
102276. .131685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.16e-75
880.00
20.06%
19.94%
49.66%
                                                                                                                                                                                                                 1. .161428
                                  78985
79085
93447
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102176
102276
131686
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred No.:
                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

I (bases 1 to 161428)

Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Margulies, E.H., Masiello, C., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maduro, N.B., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Miggins, L., Young, A., Shang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 148712 bases at least Q40 Consensus quality: 151471 bases at least Q30 Consensus quality: 151471 bases at least Q30 Insert size: 152000; agarose-fp Insert size: 160028; sum-of-contigs Quality coverage: 5.36x in Q20 bases; sum-of-contigs Quality coverage: 5.10x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4734: contig of 4734 bp in length
4834: gap of unknown length
7325: contig of 2491 bp in length
7425: contig of 2491 bp in length
12261: contig of 4836 bp in length
12361: gap of unknown length
19031: contig of 670 bp in length
19131: gap of unknown length
27849: contig of 8718 bp in length
27849: gap of unknown length
31801: contig of 3852 bp in length
40781: contig of 8880 bp in length
40781: contig of 8880 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------- Project Information
Center project name: cwp
Center clone name: 332E11
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gap of unknown 1
contig of 9429 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 8902
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                                  AC126925.1 GI:21724102
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 161428)
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59250:
68679:
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unordered pieces.
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12262
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59151
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              ACCESSION
VERSION
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δ	60 sAlaGlyGlnHisSerProLeuArgGluGluHisValThrCysVal	Db 86059 GAACATGTATGGAGACCTGGTCATGGACACGGTCCCTGAAAAGGTAGGCCCAAACCAGGT 86000
qо	87138	00 179 vo
οy	75 75	
Q	> 87078 CTAGAGGACCCAGTCTTGCTTAGTAGCCAACTCCTAAGTTGGAATCTGGAGGCCTCAC 87019	85999 ACCICAGICCCCAGAAGCCCTICIGCAGIIIGAAGCAGCIITITICAGICCCCTITIAICIC
ΟY	76	<b>は 4 4 4 日本 アメリカ 4 4 7 7 7 4 7 4 8 7 7 9 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7</b>
qa	87018	00000
QV 1	88 rLeulleProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	CTGTAATCTTTTTTTAAAGTTTGTTTATTTGAGAGAGAAAGGAAGG
8 8	88959 CCICAICCCICITAGCACIGAIGAGGIGGIAGAGAAAIIGGAGGACATITICAGCAGGA	ОУ 179 179
<u>8</u>	86	Db 85819 GAGGGAGAGTGGGGGGGAAGGCAGGAAATCTCCAGCAGATTCCCTGCTGAGTGCAGAGCC 85760
οy	113	179
qa	86839 GAGAGTATGGAGAGGTTGCTGCTGTTTCTCCCATAGGGATGTACAAGGCGGATGGAG 86780	85759 CAACGAGGGCTTGAGCTCTCAATACCGAGGGGCTTGAGCTCTAATACCGAGATCACAA
οy	, 113 113	179
qo	) 86779 GAAGGTAGAACTGAGGGGGAGGAACCTGTAGGCAGAGTGCCACGCCCCTGTAAACTGACT 86720	20
ΟŊ	113 113	P. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.
đ	86719 GGGGTGGAGTCTTTACCTGAGATCCTGCAATATTATGTATACCTGATACTCCTGTGCCTC 86660	85639 ITTGTAATCGTGGTCCTGAACTTACTAATTCTTTTCCCCCAGTGTAGGGTTTTTCCCTGT
οy	, 113 113	179
qa	> 86659 TCTGGAGACTAGGCCTTTAGCAGGTCCTCAAAAGGATGTGTGGCCCAAAGAAAG	85579 GGCTAACTCCACAAATTGGGATGGGAAGCAGTAAGATAAGGTTAAAAAGGCTTTGGTTTT
οy	, 113 113	179
qq	86599 ITTTTGTTTGAAGTGGGTTCCACACCCAGTGTGAAGCCCAACACAGGGCTTGAACTCACG 86540	85519 TTACCCTCAGTGAGTTGGAGTGCAGGTTATTGAAACTGGCCCTTGGAGCCCTAATGAAAG
QY	113 113	179
qq	86539 ACCTTGAGATCAATACCTGAGGTGAGATCAGGAATCGGATGTTTAACCGACTGGGCCACC 86480	85459 GAAGCAAGGCCAGGGTGGAGGGGACCTGGCAAGGGGGCCTGAGCTCTTCAGTTCCAT
QY	113 113	180
qa	86479 TAGGTGCCCCCACCCAGGTGCCCCCTTATTCTTAAGAATAAGAACTTAGTTTAGGTTCTT 86420	85399 CCAGGICTTTIGTATCATTGGCACAGGIGCATTTCTTCAACAGTTTCTTCTATGATAAAC
δλ	113 113	191 euArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsn
qa	96419 ATTCTGGGCAGTAGAAAAGTACTTCTGTATGCTCTAGCCCCCTTGTCTCTTGTGTGAGTC 86360	85339
γ <sub>0</sub> ς	114ArgLysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArgMe	UY 203  Db 85279 TATACGCTGGTGTGACACCTTGCCTGTAGAGGATTAGAGTTCTGTTTTCTAGGAGCCCTT 85220
<b>i</b> i	00555 CACCCTTGGCCTACTGGGGCCCTGGTGCTGCTGCTGCTGATCCAGCTGGTGGTGGGAT	Qy 205 205
중 점	128 CFTGGLYASIALametVallargGLyPheargGlyPheargyAllalyILVSargHisValleUThrWe 148	Db 85219 CCTCAAAGCCTGCTCACTCTTTCAAGTATTAATAAGGCTCTGGTATGTGGGGTA 85160
οy	148 tAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnAsp	Qy 205 205
qq	86239 GGATGACCTGGGGACCTTGTATGGACAGAACTGGCTCAATGACCAGGTGAGGAGTAGTGG	GTCGTAGGCACAAGGGATTCAGTGTTGAGTAAGGAAAACTTGCCTTTATGGAGTTAAGGG
δŏ	1.62	Qy 205 205
qq	86179 AGAAATGGGCCCAAAAGGGGATTTAGGGAGCAGGGTGTCTGGGGGCCCTCTGTTTGGGGA	TAAATAAATAGGTTAAATTTCAGCTAGTGCTAGGTGCTATGAATCACCTGAAAGGGTAAT
Qy	163GlnValMe 165	
qa	86119 GCCCTATACCTATGCTGCACTCTCCATGGCAAGTTGCCTCCAATTTTCTCCCCAGGTGAT	85039 GCAGTAGCCCGGGAGCTAGGCCCTTTAGATTGGGCGGTTTGGGGAGGCCTCTCTCT
ογ	165 tASnMetTyrGlyAspLeuValMetAspThrValProGluLys179	Qy 205 205

අු	84979	AGGTTTGAAGGCCAAGGAGCTGGCCCTGCAGATCTGGGGGAGGAGTGGTCTAAGGCAAAAG	_	
ò		000000000000000000000000000000000000000	Qy	205
전	84	AGTAGCAAGTACATGGGACCCAGAGTGAGAATGAGCATTTGAGGCACCGAAGGCCCATGT	qa 0	83839 CATCCTG
ΟY	202		Oy	205
g	84859	GGGTGTCCTGTATAGTTGGAGCATCTGAGTGGAGGGAGTGTAGTAAGAAATCCGGTCAGA	qa	83779 CCCTGGA
Οy			. Oy	205
q	84799	GTTGATCCTGTAAGGCATGGAGGAGGCAGGAGGAGGATCTTTCTT	qq 0	83719 CCCACTG
οy	205		Qy	
qa	84739	AGCCACTGAAAAGITTTAAGGAGCCTGGGAAGTCCCTCATGTTTTCAACTCCTGCTTCAT 84680		
οy	205	502	Qy	212 GluLeuL 
ΩD	84679	GTAGACTGGAAGTGGGGGGAAGAGTAGAAGCAGGCAGACTGGCCAGGGAGGG		
Qy	205	502	oy.	232 ArgArgA 
qq	84619	AAGCCTGGAGCAGGGCGCTGAGTGCAGAATGGAAGTGGCTTTCTCTAGGATAGGTTTG 84560		83539 AGGCGAC
Ωy	205	502	Qy	
q	84559	TGGGTAGAACCATGGTATTTCAGATGGGTTGGATGTGGGAATGAAGAAGAGCTAGGAAT 84500	qa 0	83480 GGTTTGA
Qy	202			
đ	84499	TGGGGAGGCCTGGGTTAGTGGCAGAAGTTACTGGGGAAAATGAGGGAACGCGTTTGGTGA 84440	qa 0	83420 AGTGGGC
Ωy	205	502	Qy	
qa	84439	TGGGGTAGGGTGGGTATCTTTTCTCCCCTCTAGTTGGGGTCCCTGCCCTCCCGCCAAAG 84380		
Qy	205	205	Oy	
qa	84379	GTGAAAAAATTGGTCTAGAGTGAAGTGGGACTGGCTCTGGCATTTTAGTTTCTGTCCCCG		83300 GAAGCAG
ογ	205	502	δλ	
qq	84319	GGTTCAGGGGCTTACACCTGCAGTGACCTGGCAGGCCCGCTTCTCCCCAGTATGGGTGGG	qa 0	83240 GTAAGTG
ογ	205		Qy	279
С	84259	TAACACAGTGGAAAGAACGTGGCCTGTGTCCCCTGTGTCCTTTCTCCTGTGCCCGTCAGA		
ΟY	202	502	Qy	280 -Asnval
qα	84199	AAGGIGCCCIACTCTCCCAGGCIGCAGTTCCATCGIFAGGCIGACTGAGAACTCCCTCAC 84140		83120 GAACGTG
QY	205	205	Oy	
ф	84139	AGGGTGGTTGTGGTAACGGGCCGACCCTTACTAGTCCTGTGCGGTGCTGTTAACGTAT 84080		83060 AGATCGG
Qy	205	205	λο i	
qq	84079	CATGGACAGGAACTAATTTAACTCTGGTAACAAACAAGTGAGATAGGCACTGTTATTCGC 84020		83000 GCTCACA
Qy	205	502	٥y	
qa	84019	AGCCTCTTACATCTAAGAGGACGGTGGCACGGAGAGCCATTCCGTAGCTCACCCGTGGTC 83960		82940 CCCCTTG
Qy	202	502	Qy	295
QQ	83959	ACAAGCTAGGAAATGGAGGAGGTGTGGGTTTAAACCCCCAGGGGGGGG		82880 TCTGGCC
QY	205	205	Šo d	111111111111111111111111111111111111111
αg		83899 GCCTGGGTTTTTAGCTATTAAGTACTCGTGCCTTTAATGTGTGGAAAGAAA	0	02020 GAACAGI

Qy	205	205
QQ	83839	CAICCIGGGGICTCAGGIGITGIGACAGIAGGICTICIGACCIGCCITCTICCCICAC 83780
Οy	205	502
qq	83779	CCCTGGAATCTACACATGCTGAACTTCACCTCACAGTGGAGGAGCTCAGCTGTGTGTG
٥y	205	205
QQ	83719	CCCACTGGGCTCCTTGTCTCCGCCTCCACTCTTAGGACCCTCGCGGCAATGGGCAGGTG 83660
Qy	206	ValAspIlePheAsnLys 211
QQ	83659	GCTCCTGCTGCTCCAACCTGACCTCTGACACCCCCCTCTAAGGTGGACATCTTCAATAAG 83600
Qy	212	GluLeuLeuLeulleProIleHisLeuGluValHisTrpSerLeulleSerValAspVal 231
qa	83599	GAGCTCCTGCTAATCCCCCATCCACCTGGAGGTGCACTGGTCCTCTGTTGACGTG 83540
οy	232	ArgargargThrIleThrTyrPheAspSerGlnargThrLeuAsnargargCysProLys 251
Ωp	83539	AGGCGACGCACCATCACCTACTTTGACTCGCAGCGCACCCTAAACCGCCGCTGCCCTAA- 83481
Qy	251	
QQ	83480	GGTTTGAGAGGGGAAAGGCGGGGGGGGGGGGGGGGGGGG
QY	251	251
QQ	83420	AGTGGGCAGGAAGGCCTGGTGCCTGGACCACTGTACCCTAGGTTCACTTGGGAAA 83361
οy	252	HislleAlaLysTyrLeuGlnAla 259
QQ	83360	CCGAGGCATCACTTCCTTTTTCCTGTCTCCATAGCATATTGCCAAGTACCTACAGGCA 83301
Οy	260	nGlyTrpLysGlyTyrPheLysMe
qq	83300	GAAGCAGTGAAGAAAGACGGGCTGGATTTCCACCAGGGCTGGAAAGGTTACTTCAAAATG 83241
δy	279	279
οqα	83240	GTAAGTGTCTGGAGGGAGGGGTACAGGTGGTGATGGTGGTGGTAGAGGAGCGGTAGGAGG 83181
οy	279	279
qq	83180	AAGAAGTGGAAGCCACACCCCGAGGAGCGTCCAGGTGAAGGACTTCTTTTTTTT
Οy	280	-AsnyalalaargGlnasnasnAspSeraspCysGlyAlaPheValLeu 295
QQ	83120	GAACGTGGCCAGGAATAATGACAGTGACTGTGGTGCCTTTGTGTTACAGGTAAGCAG 83061
٥y	295	295
qq	83060	AGATCGGTGGGGTTAAAAGGTTTGGTAAGGAGGTGGGAGGCTGTTCCACCTCTCTGGTTTG 83001
Qy	295	295
qq	83000	GCTCACAGGCACTTGTGAAGCAGAGAAGCTTAGGTGTTAGTGTGCAGAAACTCGGAT 82941
Οy	295	295
qq	82940	CCCCTTGGTCTCCCCGGCTTCCCCGGGCCCACACTTGGCCTGGGTCTCTTGGTCCTTGGTC 82881
ΟŸ	295	295
QQ	82880	TCTGGCCCTGGTACAGTTGCTTCCCAACCCCCAGTGCAAAGCATTTTCTTCAGGTATCGA 82821
οy	295	295
qq	82820	GAACAGTGACTCTAGAGTCAGGCTTTGAGCCTTAGGCTATGGGACGTTGGCTTTGTGTGT 82761

1107 others gap of unknown length contig of 16900 bp in length gap of unknown length contig of 20469 bp in length of 42025 bp in length. in length of 17079 bp in length unknown length of 8366 bp in length bp in length bp in length length length length length unknown length unknown length gap of unknown length Length:
Matches:
Conservative:
Mismatches:
Indels: of 15520 bp vector\_side:right" a 37393 c 36616 g 39259 t unknown of 7180 unknown of 9325 1. .153553 /organism="Bos taurus" /db\_xref="taxon:9913" /clone="RP42-45D24" /clone\_lib="RP42" /note="assembly\_fragment" 2413. .5841 /note="assembly\_fragment" unknown unknown 2494 of 7264 5942. 8435 /note="assembly\_fragment" 8536. 15799 /note="assembly\_fragment" 15900, .25224 /note="assembly\_fragment" 25325. .32504 /note="assembly\_fragment" 'note="assembly\_fragment" note="assembly\_fragment" /note="assembly\_fragment" 73870. .90850 /note="assembly\_fragment" 111529. 153553 'note="assembly\_fragment" 'note="assembly\_fragment contig gap of contig gap of contig gap of contig gap of gap of contig gap of contig gap of contig gap of contig Location/Qualifiers contig clone\_end:T7 vector\_side:left"

qq	36532	:::	ı
δ	20	aproproAspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGl 40	
QQ	36472		
Qy Dp	40	nGluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLy 60 	
Qy	9		
g	36352		
οy	77	11	
qq	36292	: CTCCGGGATCTCGTCTTTCCCCTCAGCTGAGTGTGAGATCGGAGTCTGGAGTCTCACTTT 36233	
οy	78		
ф	36232	TCTCTCTTCCCTCCACTCAGGCATCTTGGATGAATTCCTTCAGACTTACGGCAGCCTCAT 36173	
δλ	6 5	eProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGluBheSe 110	
2		AUCUCTUAGUAUTGATGAGGTAGTGGAGAAACTAGAGGACATTTTCCAGCAGGAGTTCTC 36	
à à	110	rThrProSer	
2	30112	TIGCACCTICCAGGTGAGGCATGAAAGAGATGCCCTTTGGAAGAGGGCTGGGACCTGAGAG 36053	
οy	113	113	
qq	36052	ATGGGGAGAGAATGCTGCTTTTTCTCCCATAGGGATGTAGTCGGGGAGGAGGAGGAGAA 35993	
δy	113	113	
Dp	35992	GCTAGAACTGAAGGGGAGGAATCTGCAGACAAGGTGCCAAGGCCCCGTGAGCCACCCGGG 35933	
δy	113	113	
QQ	35932	AGGGCCTTTACCTGGGACCCTGAAATACCATGTGGACCTAAGTATTCCTATGCTTCTTAC 35873	
οy	113	113	
QQ	35872	AGGGGAGTGTGCCTTTAGCAAGTCCTCAAAAGGACCCATGACCCAAAGAAAAAGTTTTAG 35813	
ΟY	113	113	
QQ	35812	ATTCTTATTCTAGGCAGTAGAAGGTACTTCTGTGTGCCCAAGCCACCGCCCGGTCCCCAA 35753	
Qγ	114		
g	35752	TCTCTTGCATGACTCAACCCTTGGCCTACCCAGGAGGGCCTGGTGGTGCTGCAGTTGATCCA 35693	
δy	123	nSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArgValAjaTyrLysAr 143	
qq	35692		
QY Db	143	gHisVilleuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnAsp 162 	
οy	162	162	
Ob	35572	GGTAAGGAGGTGTGGAGAAACAGGCCCAAGAGTAGGTTTGGGGAACAATGTATTTGGGGC 35	
ΩŽ	162	162	
qq	35512	CCTCTCTGGGGAAGCCCTGTACCCATGCCACCCTCCATGGCAAGTGGCCTCCCGTC 35453	
οy	163	GInValMetAsnWetTyrGlyAspLeuValMetAspThrValProGluLys 179	

QΩ	35452	TTCTCCTCAGGTGATGAACATGTACGGAGACCTGGTCATGGACACAGTCCCTGAAAAGGT	35393
οy	179		179
QQ	35392	AGGCCTAACTAGATACTTCAGTCCCTGGAAAAACTTTTGAAGTTTTAAGCAGCTTTTTCA ;	35333
Qy	179		179
Db	35332	GTCTCTCATGTCTTCCATTTTACGTAAAGAGGGTCTTTCTT	35273
οy	179		179
QQ	35272	AGGTAATTTGTTAAATTTCAAATTTGTAATCTTGGTCCTGAACTTTTCTAGTCCTTTCCCC	35213
Qy	179		179
qq	35212	TAGTCTGTAGTGTTTTTCCCCAATGGCTAGCCCCACAAATCAGGGTGGGAACTTATAAGA 3	35153
ΟY	179		179
qq	35152	TGAGGTTGAAAACAGTTTGTGCTTTTTACCTTTAGTAAGTTGGACTGGAGTTTGTGGAAA	35093
Qy	179		179
qq	35092	CCAGTCCTTAGAGCCGTGATGAAATGGAGGCGGGGGAGAGGACACACGTGGCGGAGGG 3	35033
Qy	180		184
QQ	35032	CCTGCGGTCTGTTGATTCCACCTGGCTCTTTTGTATCGTTGGCACAGGTGCATTTTTTTT	34973
Ωy	184	snSerPhePheTyrAspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThrL ;	204
QQ	34972		34913
Qy	204		205
qq	34912	 	34853
Οy	205		205
qq	34852	TTCCTGTGAATCCTTTCCCCAGCTCTGTTCATTCAGACTTTCAAGTATTTATT	34793
Ωy	205		205
qq	34792	TTTTGTGTGCCAGGTACTGTTCTGGGCATTAAGGATACAGTATTAAATAAGGAAAACTTA 3	34733
Qy	205		205
Ор	34732	TTGCCTTTTAGGGGGTGAGAATCAATAAGCCAGTTAAAGTACAGGTAGTGATAATTTGCTG	34673
Qy	205		205
QC	34672	TAAACAAAACAGTAATGTGGTAGCATGGGGCTGGGTACTTCAGATAGGGTGGTTTGGGAA	34613
Qy	205		205
QΩ	34612	GGCTTCTTTAGCTGATACTTTAGTGAGCCAGCCCTGTGCACATCTGGGCAAGGGTGTAC	34553
Qy	205		205
QQ	34552	TAAGCAAAGGGAACACCGGGAACATGGGATACAGAGCAAGAAAGA	34493
Qy	205		205
QQ	34492	AGGGCCCGTGTGGCTGTGGTTGGAGCAGAACGAGCAAAAGGAAAAAAACGATAGAAA	34433
γo.	205		205
QO	34432	ATTTGGTCAGAGAGTAGATCATGTGAGGCGTGGAGGCCAGGTCAACCAGGGTAGATTTTA 3	34373
Qy	205		205
Q	34372	TTCTTTGTGGTCTAAGAAGCCATTGAAGAGTGTCGAGCAATCTAGGAAGTGACTCACGTT 3	34313

			QY	206	ValAspile
ΟŊ	205	5 205	2	22727	
QQ	34312	2 TTAAACTCCTGTTTCGGCGATGGAAAGGGGGCAAGAGTGGAAGCAGGCAG	2		
Qy	205	5 205	δo i	226	LeulleSer
qa	34252	2 GTAGCTGAGAAGTCCTGATGAGAACTTGGACCAGAGTGGTCAGTGTGGAAATATTGATA 34193	an		CICAICICI
Qy	205	5 205	δŏ		AsnArgArg(
qa	34192	2 GTAGTAGTTTTATTTAGGGTAGCTCTTGCAGGTAGAACCAATAGGACTTTCTGATGGATT 34133	q <sub>Q</sub>		AACCGCCGC
Q	205	5	Οy	251	• • • • • • • •
qq	34132	2. GGACATGAGAGATGAGGAAAAGATAGCAATCAAGGATGATGTCTAGGTTTTTGGCCTAAG 34073	QQ	33052	ATCCAGTGG
ΟŶ	205	5 205	δλ	251	
đ	34072	2 ITACTGGGGAATATAATTAAGGCGGAGGGAGCAGCTTTGGTGGGGTGGGAAAGAGTTCT 34013	ag O	32992	GGCTTGGTG
Ωy	205	5 205	δλ	252	
qa	34012	2 TITCTCCATTCTGATTAGTTTACCTGTCCTCTGATTCAAAGGCCAGGAAATTCCAATAGT 33953	QQ	32932	CTTCTTTCC
οy	205	5 205	ΟŊ	264	SASPArgLe
· 6	33952	2 GAGGTAGGGCTATTGCCTCTAGCATTTCTTAATTCCTGTTTCCCTGTAGAGGTGGGGTGA 33893	QC	32872	AGACCGGCT
οy	205	5 205	٥y	279	
q	33892	2 CCTGCATCGGAAAGAACTTGGCTTTCTATATGCCTGTGTCCTGTGTTTAAATTCCACCTC 33833	qa	32812	GAGGTTTAA
·δ	205		Qy	280	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
· da	33832	TGTCATCTCTTATTCTCTCACCTTGAGCAAGTTGCTTTACTTTTCCAAGGCAGTTTCCT	QD	32752	CACATAGGG
ò			Qy	284	GlnAsnAsn/
3 2	,		qa	32692	CAGAATAAT
3 8		CALGAGRACT TIGIT L'ORGGATIGE TGIGITRACTGACTGAGCATCTGATTAGGTGCCATG	RES	RESULT 11	
Š	CO <b>7</b>	607	LOC	AKUUU923 LOCUS	AK00092
qa	33	2 CATTGTTCTTAGAGTATTGTGGATATCAACTAGTTCAATCTGTGTAACAAACA	DEF	DEFINITION	
Qy	205	5 205	VER	VERSION	AK00092
q	33652	2 ATAGATACTGTTATTTTCAGTCTTACAGAAAAGAAATTGAGGTATAGAGTTACTAAGTA 33593	SOL	SOURCE	Homo sar
οy	205	5 205	O	ORGANISM	Homo sar
đ	33592	2 ACTTGCTTAGTAACCCAAGTAACTTAACTAAGTAACTTAGTAACCCAGGTTACTTAC			Eukaryor Mammalia
Ωy	205	5 205	KEF	KEFERENCE AUTHORS	Isogai,
q	33532	2 CTTGGGTCATACATGGAGGTGGAGTTTGAACCTTGAGAGTCTGACTCCAGGATCTTGA 33473			Tanase,
Ωy	205	5 205	,		Arita,M Wakamate
qa	33472	2 ACCTACTAAGCATTIGTACCTTTAATGTGTAAAAGTACCTGGCCTATCCTGGGCCCTCC 33413	,	TITLE	NEDO hur Unpublis
٥y	202	5 205	KEN	FERENCE	z (base Isogai,
QΩ	33412	2 AGTGTTTGTTCTGTACCACCTCCTCTGTTTGCTTTCCTCCTTAAGCCCAAGAATCCGAA 33353	F (3	TITLE JOURNAL	Submitt
٥y	205	5 205	Ĉ	Į.	(E-mail
q	33352	2 CATCCAGATGCTGGGCCTTGCCTCACGGTCCAGGGGCTAGGAGTTGAGTTCTTCCACTTA 33293	Š	COMMENT	Internat
QΣ	205	5 205			construction
qa		33292 GCTTCTTGCCTGCTCCTCCTGTGCTATCTTACCTGACCTCCAGCCCTGCCTTAG 33233			etc.) ar

ValaspilePheasnLysGluLeuLeuLeuIleProileHisLeuGluValHisTrpSer 225	LeulleSerValAspvalArgArgArgThrileThrTyrPheAspSerGlnArgThrLeu 245	ASBRAGGY STROLYS 251	251	ATCCAGTGGCAAGGCATTTCAGGCAGAAGGTTGGGTTTTGGGTCTCTGATGAGCAACCTG 32993	251	GGCTTGGTGCCTGTGACCAGCACGTTGGGTTCAGTTGGGAAATGCAGAGGCTCACTTC 32933		CTTCTTTCCTCCAT	sAspargLeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMet	279	GAGGTTTAAGCAGGGTTGAGGTGGTGGTGGTGGTAGGAGGCAGAAGCTGAAGCTATA 32753	283	CACATAGGGTCTCCAGGAGAAGGGCTTACCTTC	GInAsnAsnAspSerAspCysGlyAlaPheValLeuGInTyrCysLysHis 300 	AKO00923  AKO00923  AKO00923  N Homo sapiens CDNA FLJ10061 fis, clone HEMBA1001413.  AKO00923.1 G1:7021892  Oligo capping; fis (full insert sequence).  HOMO sapiens embryo, 10 weeks whole embryo, mainly head cDNA to homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to homo sapiens.  E Jacone_lib:HEMBA1 clone:HEMBA1001413.  SM HOMO Sapiens  E Liscari, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Arita,M., Nabekura,Y., Togiya,S., Komai,F., Hara,H., Takeuchi,K.,  Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,  NEDO human cDNA sequencing project  Unpublished  E J (bases I to 1578)  E J (chases I to 1578)  E J (chase I to 1578)
33232	226 33172	246 33112	251	33052	251	32992	252	32932	264 32872	279	32812	280	32752	284 32692	RESULT 11 LOCUS LOCUS DEFINITION VECCESSION VERYWORS SOURCE ORGANISM ORGANISM TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE COMMENT
Qy	Qy Db	Oy Db	Οy	QQ	ΟŸ	qq	δy	qa	Qy	οy	Ωp	٥y	QQ	Qy Db	RES ACC LOCK KERK KERK KERK KERK KERK KERK KERK KE

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NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 257644)
Worley, K.C.
Direct Submission
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Contact: hgsc-help@bcm.tmc.edu
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Δυυ/ bp mRNA linear PRI 13-JUN-2001 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R. Sitel: Draili (CACTOTGTG)
Description: lst strand cDNA was primed with an oligo(dT) primer
Description: lst strand cDNA was primed with an oligo(dT) primer
[ATGTGGCGTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with Sfil and size selection was performed to
exclude fragments <1.5b. The Sfil digested PCR product was cloned
into distinct Draili sites of pME18S-FL3. XhoI sites just outside
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
oligo capping; fis (full insert sequence).
Macaca fascicularis adult male temporal lobe right cDNA to mRNA,
clone_lib:macaque brain cDNA library QtrA clone:QtrA-13616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K. Isolation of full-length cDNA clones from macaque brain cDNA
                                                                    :::||| |||||||||:::|||| 206498 AGACAAAGGCTATAAAGAGTTAAGAGAGTGGACTAAGAAGGTTTG
                                                                                                                                    206558 TITAAAAAGGGCTTCTGTTGATTCCCATCCACCTGGAGGTCCACTGGTCTCTGATTACT
                                                                                                                 PheAsnLysGluLeuLeuLeuIleProIleHisLeuGluValHisTrpSerLeuIleSer
                                                                                                                                                                                     229 ValAspValArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArgArg
                                                                                                                                                                                                                                                                                  PheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsnAspSer
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                                                189' AspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsnValAspIle
                                                                                                                                                                                                                                                    249 CysProLysHisIleAlaLysTyrLeuGlnAlaGluAlaValLysLysAspArgLeuAsp

    (bases 1 to 2007)
    Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S. Direct Submission

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PME18S-FL3 (Acc.No. AB009864)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAspLeuValMetAspThrValProGluLysValHisPhePheAsnSerPhePheTyr 188
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                    (Sugano et al., , Institute of Medical Science, University of Tokyo).
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can be used to isolate the cDNA insert.
                                                                                                                                /tissue_type="temporal lobe right"
/clone_lib="macaque brain cDNA library QtrA"
/dev_stage="adult"
1140. .1442
                                                                            1. .2007
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QtrA-13616"
/sex="male"
                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
          were constructed by oligo-capping method
                                       Custom primer used for sequencing (5' end primer [CTGCTCTAAAAGCTGGG]; 3' end primer [CGACCTGCAGCTCGAGCACA]).
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 19 Row: e Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1830)
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Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Center code: BAM HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garci
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                               982 CCCATCATGAGCCGAATAAAAGGGGGTCAGTTAGAATTTGTATTCTAGGGAGTAGTAGGT 1041
                                                                                                                                                                                                         1042 ATTTCTGTGTGCCCCAGCTGCATCAACTTTTGTGTGACTCCACCCTTGGCCTACTCAGGA 1101
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1830 bp mRNA linear P.
Homo sapiens, clone IMAGE:3448367, mRNA, partial cds.
BC008589
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (24 MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LinL at: http://image.llnl.gov Series: IRAK Plate: 33 Row: i.Column: I This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCU30705 2793 bp mRNA linear PRI 30-MAY-2
HOMO sapiens, clone MGC:27076 IMAGE:4824344, mRNA, complete cds.
BC030705
                                                     1324 TCATTTTATGATTCCCAAGGCATTCATTTTAAGTTTTGTGTAGAGAATATAAGAAAGTAT 1383
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                                                                                                                  LeuGlnAlaGluAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGlyTyr 276
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ThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTyr 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Enail: cgapbs-refmail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) &
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
                                                                                                                                                     GTTACGAAGTGTATTCCACAACAGAAAAACGACAGTGACTGTGGGAGTCTTTGTGCTCAG
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Length:
Matches:
Conservative:
Mismatches:
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(1-2793)US-09-848-852A-3 (1-332) x BC030705

1775 ValValGluLysLeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGly 116 96 58 GlyGluLysAlaGlyGlnHisSerProLeuArgGluGluHisValThr---CysValGln 76 6 ò q g δ oy Db

1776

156 LeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGly 136 PheArgValAlaTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGly 117 137 Qy Db QY

176 157 GlnAsnTrpLeuAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrVal

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ProGluLysValHisPheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyr 196 177

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PheLysMetAsnValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGln

316 TyrCysLysHisLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLys 297 ò a

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GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INFURION: Nucleotide Sequence of Escherichia Patent No. 6316609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Ave, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY/ACENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/976,259 FILING DATE: Herewith
US-09-134-001C-1230
US-08-531-927B-8
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US-09-313-927-205
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/ina/5A_COMB.seq:*/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                                                            - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-302-812-38
US-09-511-477-38
US-09-511-507-38
US-09-356-952-12
US-09-134-001C-405
                                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-976-259-58
US-08-75-709-2
US-08-752-229-2
US-09-534-638-1
US-08-755-709-1
US-08-752-929-1
US-08-090-793-1
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7.0
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum Match 100%
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length: 2000000000
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Match
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Maximum DB seq
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Perfect score:
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Database :

Result

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2836, Ap 6, Appli

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Sequence

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STREET: B.C. Street, N.W., Suite 500 CITY: Washington
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAX-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAX-1992
ATTORNEY/AGENT INFORMATION:
                                                                                    RESULT 2
18-08-375-709-2
Sequence 2, Application US/08375709
Patent No. 5683898
                                                                                                                                                                                                                                                                                                                                                               STAUE:
COUNTRY: USA
COUNTRY: 20007-5109
ZIP: 20007-5109
COMPUTER READABLE FORM:
TITLE TYPE: FLORBY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1983 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECHIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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(202)672-5399
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                    287 AspSerAspCys 290
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APPLICANT: YAZAWA
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Best Local Similarity:
Query Match:
DB:
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LOCATION:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 ProGluLysValHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyr 196
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                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValVal 98
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Matches:
Conservative:
Mismatches:
Indels:
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 4835 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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US-08-976-259-58
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APPLICANT: TAMADA, AKIKO
APPLICANT: KATO, Seishi
APPLICANT: KATO, Seishi
TIPLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of
TITLE OF INVENTION: Eiscosapentaenoic Acid
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1983
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ORGANISM: Shewanella putrefaciens SCRC-2874 (FERM ORGANISM: BP-1625)
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,709
FILING DATE: 20-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: WEGNER, Harold C. REGISTRATION NUMBER: 52,258
REFERENCE/DOCKET NUMBER: 53466/150/AAOK
TELECOMMUNICATION INFORMATION:
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GENERAL INFORMATION:
APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAMADA, Akiko
APPLICANT: YAMADA, Akiko
APPLICANT: KATO, Seishi
APPLICANT: KATO, Seishi
APPLICANT: KONDO, Kiyosi
TITLE OF INVEWITION: Gene Coding for Eicosapentaenoic Acid Synthesizing
TITLE OF INVEWITION: Enzymes and Process for Production of Eiscosapentaenoic
TITLE OF INVEWITION: Acid
NUMBER OF SEOURNES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,929
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,258
REFRENCE/DOCKET NUMBER: 53466/150/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
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Gaps:
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APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-3AN-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               Sequence 2, Application US/08752929
Patent No. 5798259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEEX: 904136
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1983 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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(202)672-5399
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CITY: Washington
STATE: D.C.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------TACAAGACGTGGCATACCAATGGTTACCACGGCACT-----TATAGCCA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                978 GIGGTCAAAAGATATCAACGAAATGATCAATGCCTTTGGTCAAGATGTCGAAGTGCTGTT 1037
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                                                                                                                                                                                   597 CTCA------GATAACATCACTAAAGAAATTGTCGATGAGAACTACT 638
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                                              GlyThrIleTrp-AlaArgArgGlyAlaHisLeuAlaProProAspAlaSerIleLeuIl
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US-09-848-852A-3 (1-332) x US-08-752-929-2 (1-1983)
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                                                                                                               GENERAL INFORMATION:
APPLICANT: Panula, Pertti A.J.
APPLICANT: Brandt, Annika
APPLICANT: Brandt, Annika
TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use;
TITLE OF INVENTION: for therapy and diagnosis
FILE REFERENCE: 2530-104
CURRENT APPLICATION NUMBER: US/09/534,638
CURRENT FILING DATE: 2000-03-27
EARLIER FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 2.2
SOFTWARE: PatentIn Ver. 2.1
1422 TGTTGCAACGGCATTAAATAAGGTGGTGATGGCCGAGCCAGAAAATGACTCC 1473
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Mismatches:
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                                     RESULT 4
US-09-534-638-1/c
; Sequence 1, Application US/09534638
; Patent No. 6320038
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93.00
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Best Local Similarity:
Query Match:
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                                                                                                                                              6759 TGCCGGTAACGCCATGAGCCGCCGCGCGCTTATCAATACGGCGCAACACTGGGCAAAAA 6818
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                                                                      ------GATAACATCACTAAAGAAATTGTCGATGAGAACGTACT 6758
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                                     eSerAsnValCysSerIleGlyAspHisValAlaGlnGluLeuPheGlnGlySerAspLe
                                                                                                          uGly-------MetAlaGluGluAlaGluArgProGlyGluLysAlaGlyGlnHi
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US-08-752-929-1
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                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of
TITLE OF INVENTION: Eiscosapentaenoic Acid
GlyThrIleTrp-AlaArgArgGlyAlaHisLeuAlaProProAspAlaSerIleLeuIl 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTE: EALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/375,709
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
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Matches:
Conservative:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION UNDMER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION UNDMER:
APPLICATION UNDMER: JP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                              Sequence 1, Application US/08375709
Patent No. 5683898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 5346
TELECOMMUNICATION INFORMATION:
TELEPAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                      Kazunaga
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TYPE: nucleic acid
STRANDEDNESS: double
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93.00
32.96%
20.95%
5.25%
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APPLICANT: YAWADA, AKIKO
APPLICANT: KATO, Seishi
APPLICANT: KONDO, Kiyosi
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                              GENERAL INFORMATION:
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                                                                      GAT 3237
                                  Asp 268
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GENERAL INFORMATION:
APPLICANT: Calgene, LLC
TITLE OF INVENTION: Production of polyunsaturated fatty acids by expression
TITLE OF INVENTION: of polyketide-like synthesis genes in plants
FILE REFERENCE: CGNE.131.01US
                                                                                                                   6879 CGTCGCCCCA----GACTACACCTTAAACAGTGAAGGCAAATGGGAAACGCTGACG-- 6930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TACAAGACGTGGCATACCAATGGTTACCACGGCACT-----TATAGCCA 7370
                                                                                                                                                                                                                                                                                                           ------ATTGATGGTCTAGAGATGGTGTTTATGGATGCCTCGGGCACCGGAGCTGA 6980
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                                           6759 TGCCGGTAACGCCATGAGCCGCCGCGCAGCTTATCAATACGGCGCAACACTGGGCAAACA
  --- MetAlaGluGluAlaGluArgProGlyGluLysAlaGlyGlnHi
                                                                                       ----SerProLeuArgGluGluHisValThrCy
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Patent No. 6140486
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                                                       APPLICANT: YAMADA, Akiko
APPLICANT: KATO, Seishi
APPLICANT: KATO, Seishi
TTLEON: KONDO, Kiyosi
TITLE OF INVENTION: Gene Coding for Eicosapentaenoic Acid Synthesizing
TITLE OF INVENTION: Enzymes and Process for Production of Eiscosapentaenoic
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
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Matches:
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-JAN-1995
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/752,929
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFRENCE/DOCKET NUMBER: 5346/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
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TELEFAX: (201, 1)
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 37895 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                       GENERAL INFORMATION:
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COUNTRY:
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Patent No.
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6879 CGTCGCCCCA-----GACTACACCTTAAACAGTGAAGGCAAATGGGAAACGCTGACG-- 6930
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CTATCAAGGTATGCACAACATTAATACGCTGCGGGGGGTAAAGTACGTGATGCGCTCAA 7097
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                  Gaps:
                                                                                                           ; TYPE: DNA
; ORGANISM: Shewanella putrefaciens
US-09-090-793-1
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Best Local Similarity:
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Sequence 38, Application US/09302812B

Sequence 38, Application US/09302812B

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Sequence 38, Application US/09302812B

SEQUENCE NO. 1333148

APPLICANT: JACOBSON, Myron K.

APPLICANT: JACOBSON, Elaine L.

APPLICANT: APPLICANT: ALN, Jean-Christophe

TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACT

TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACT

TITLE OF INVENTION: THE PROTEINS AND SEASON OF SEASON
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sAsnValAsp---IlePheAsnLysGluLeuLeuLeuIleProIleHisLeuGluValHi 223
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                                                                      7371 TAACGCTAAAGCGGTTTATAACAAGTATCTA----
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26884 ATCGATGAA-----
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89.50
41.51%
20.38%
5.05%
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Db 26755AAAACTAAATGGGGATCTTCAAAAACAATTTTGTGGCCATAT 26705 Qy 152GlythrLeuTyrGlyGlnasnTrpLeu 160	Qy 59 GluLysalaGlyGlnHisSerProLeuargGluGluHisValThrCysValGlnSerIle 78             26932 GaaaaaGaTCAaaaaATTAaaaAGAAGAaGTTGAGAAATTA 26885
Db 26704 CCGGTTAACGGTGCGGGAATATTAATTGGTGATGAAACACCGAAACAAGAGAAGTTG 26645	Qy 79 LeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValVal 98
Oy 161 AsnAspGlnValMetAsnMet	TGAACAAGAAGAT TGAACAAGAAGATATATATATATATATATATATATATATATATA
	26857 CTAGCTGAAATGCAAATTCGAAATAAAAGCAGAGAGCAGAAGCTAGAAGTTG
Db 26584 CACTTGCTGGAAACTATTGACAAGATCATAGTCACGTTTTCTTATTTCAAGATCCT 26525  Qy 190	Qy 115 LysGlyLeuValLeuGlnLeuTleGlnSerTyrGlnArgMetProGlyAsnAlaMetVal 134
Db 26524 ATACTTATAACAAAAAGATGGAAGACAACAACAGATCATTCAAAAACTTGAAAACGAA 26465	Qy 135 ArgGlyPheArgValAlaTyrLysArgHisValLeuThrMetAspAspLeu 151
<pre>Qy 199 ValLysArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuLleProIle 218</pre>	Db 26755AAAACTAAATATGAGGATCTTCAAAAACAATTTTATGATTTGCGCCATAT 26705  Qy 152GlyThrLeuTyrGlyGlnAsnTrpLeu 160
219 HisLeuGluValHisTrpSerLeulleSerValAspValArgArgArgThrlleThr	26704 CCGGTTAACGGTTACGGTGGATATTAATTGGTGATGAAACACCGAAACAAGAAGTTG
Db 26404 GAAAACAAAGATGATTATCTCTTAGTGACAGTGGAATTCCAAAAAAGAAAATATTCTG 26345 Oy 238 TyrPheAsp-SerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTy 256	Qy 161 AsnaspGlnValMetAsnMetTyrGlyAspLeu 171
26344 TTTCCGAACTCAAGAAAAGAATGAAGAGATAAAATGCTTCATCTTCATGTT	172ValmetAspThrValProGluLysValHisPhePheAsnSerPhePheTyrAsp 189
uy zoo freduzinaladaranluyasharpargledaksprheniscingiyirpluyggiyiy z/6   ::::::: ::::::::::::::::::::::::::::	DD Z6584 CACTIGCIGGAAACIATIGACAAGAICAIAGICACGITITCICITITATITCAAGGAICCI Z6525 Qy 190
Qy 276 rPheLysMetAsn 280	DD 26524 ATACTTATAACAAAAAAGATGGAAGACAACAACAGATCATTCAAAAACTTGAAGACGAA 26465
Db 26245 TrGGAACTTCAAC 26233	199 ValLysArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeulleProIle
RESULT 977-38/C 15-09-511-477-38/C ; Sequence 38, Application US/09511477	DD 26464 GTTGACTATCTTACGAAAAACTTGGAAAGTTTGAATCCATCGCAGCTGGTTACATCTTG 26405 Qy 219 HisLeuGluValHisTrpSerLeuIleSerValAspValArgArgArgThrIleThr 237
; Patent No. 6337202 ; GENERAL INFORMATION:	26404
ANT: JACOBSON, Myron K. ANT: JACOBSON, Elaine L. ANT: AME, Jean-Christophe CANT: LIN, Winston	Qy 238 TyrPheAsp-SerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTy 256 :::::   ::::       :::::::::::::::::::
	256 rLeuGlnAlaGluAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGlyTy :::::::: ::::::::::::::::::::::::::
; FILE REFERENCE: NIAD 201 ; CURRENT APPLICATION NUMBER: US/09/511,477 ; CURRENT FILING DATE: 2000-02-23	Db 26284 TATCAGAAGGATAGTATTGAAAAAGTCATGGAGAAATT 26246 Qy 276 rPheLysMetasn 280
: PRIOR APPLICATION NUMBER: 09/302,812 ; PRIOR FILING DATE: 199-04-30 ; NUMBER OF SEO ID NOS: 38	26245
SEQ ID NO 38 LENGTH: 29793 TYPE: DNA ORGANISM: Caenorhabadi	SES-S
US-09-511-477-38	APPLICANT: APPLICANT:
	APPLICANT: AME, UGAIN ULISTOPHES TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREAC TITLE OF INVENTION: THEREWITH TITLE OF INVENTION: THEREWITH TITLE OF INVENTION: THEREWITH CHIRDRAN ADDITIONAL NUMBER: 114,009,511,507
09-848-852A-3 (1-332) x US-09-511-477-38 (1-29793)	CURRENT FILING DATE: 2000-02-23 PRIOR APPLICATION NUMBER: 09/302,812

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValLysArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuIleProIle 218
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                                                                                                                                                                                                                                                                                                                                                                                     -----GluLysLeuGluAspIlePheGlnGlnGluPheSerThrProSerArg-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --------GlyThrLeuTyrGly-------GlnAsnTrpLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26797 AAGAAGTTGTTGATAATGAGAAATGAAGATTTCTCAATTCTC--------
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54
56
81
74
13
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                     ORGANISM: Caenorhabaditis elegans
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  1999-04-30
                                                                                                                                           33.3
89.50
41.51%
20.38%
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PRIOR FILLING DATE: 1999
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 38
LENGTH: 29793
TYPE: DNA
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                                                                                                                                                                 Percent Similarity:
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Query Match:
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Pred. No.:
                                                                                               US-09-511-507-38
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RESULT 11
US-09-356-952-12
S-9-356-952-12
Sequence 12, Application US/09356952
Fatent No. 6117663
Sequence 12, Application US/09356952
Sequence 12, Application US/09356952
Sequence 12, Application Sequence 13, Applicant Borragarit, S. M.
APPLICANT BOR-Sogi, Dafna
APPLICANT COLe, Philip
APPLICANT KULIYAN, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
TITLE REPERENCE: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT PILING DATE: 1999-07-19
SEARLIER FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------AspThrValProGluLysValHisPhePheAsnSerPhePhe 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrTyrGlySerLeulleProLeuSerThrAspGluValValGluLysLeuGluAspIle 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32316 AATCCTTTACGCGATGAGTACTTCACAATATTGGAAGATGAACTGAAAGGTTTTTTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 SerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAspGluPheLeuGln
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Mismatches:
Indels:
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88.50
34.46%
19.93%
4.99%
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Best Local Similarity:
Query Match:
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TYPE: DNA
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US-09-356-952-12
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us-09-848-852a-3.rni

Qy 204 LysasnValaspIlePheasnLysGluLeuLeuLeulleProIleHisLeuGluValHis 223	Db 2806 CGTACTTTCAATGAAGTAGAAGTATATCATCTAAATGAACGG 2853
224 TrpSerLeulleSerValAspValArgArgArgThrlleThrTyrPheAspSerGlnArg 243 1	Qy 191 LeuargThrLysGlyTyraspGlyValLys
244 ThrLeuAsnArgArgCysProLysHisileAlaLysTyrLeuGlnAlaGluAlaValLys 32802 aCCAMMENTALANANANANANANANANANANANANANANANANANAN	Qy 206 ValaspilePheAsnLysGlu
2502 ROCKTITICSHURGHANNINGKANNINGKANNINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKANINGKA	Qy 220LeuGluValHisTrpSerLeuileSerValAspValArgArgThrileThr 237 
284 GlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHisLeu 301	Qy 238 TyrPheAspSerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTyrLeu 257
302AlaLeuSerGlnProPheSerPheThrGlnGlnAsp 313	Qy 258 GlnAlaGluAlayalLysLysAspArgLeuAspPheHisGlnGly-TrpLysGl 275 
SULT 12 -09-134-001C-405	Qy 275 yTyrPhelysMetasnValalaargGlnasnAsnAsnAspGy 290           ::   :: :::   bb 3133 TTACTTCAAATTGAATTCAATGTTGCAATCACTACCAAAACGTTAACTAAACGT 3192
Sequence 40.5, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al	Qy 290 sGlyalaPheValLeuGlnTyrCysLysHisLeuAlaLeuSerGlnPr 306 :::
TITLE OF INVENTION: NOCEEL ACLD AND AMAINO ACLD SEQUENCES KELATING TO STAPHYLOCOCCUS; FILE REFERENCE: GTC-007 CURRENT APPLICATION UMBER: US/09/134,001C	Qy 306 oPheSerPheThrGlnGlnAspWetProLysLeuArgArgGlnIle 321 
; PRIOR APPLICATION WIMBER: US 60/064,964 ; PRIOR FILING DATE: 1997-11-08 ; PRIOR FILING DATE: 1997-08-14 ; PRIOR FILING DATE: 1997-08-14 ; SEQ ID NOS: 5674 ; SEQ ID NO 405	RESULT 13 US-09-134-001C-1230 ; Sequence 1230, Application US/09134001C ; Patent No. 6380370 ; GENERAL INFORMATION: ; APPLICANT: Lynn Doucette-Stamm et al
LO.	; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: GTC-007 ; CURRENT APPLICATION NUMBER: US/09/134,001C
Alignment Scores: 1.97 Length: 3456 Score: 87.50 Matches: 60 Percent Similarity: 43.36% Conservative: 51 Best Local Similarity: 23.44% Mismatches: 96 Ouery Match: 4.94% Indels: 50 DB: 4 Gaps: 14	; CURRENT FILING DATE: 1998-08-13 ; PRIOR APPLICATION NUMBER: US 60/064,964 ; PRIOR FILING DATE: 1997-11-08 ; PRIOR APPLICATION NUMBER: US 60/055,779 ; NUMBER OF SEQ ID NOS: 5674 ; SEQ ID NO 1230 ; LENGTH: 2184
US-09-848-852A-3 (1-332) x US-09-134-001C-405 (1-3456)	; TYPE: DNA ; ORGANISM: Staphylococcus epidermidis
Oy 98 ValGluLysLeuGluAspIlePheGlnGluPheSerThrProSerArgLysGlyLeu 117 ::: :::    :::    :::	ment Scores: 1.47 Length:
OY 118 ValLeuGinLeuileGinSerTyrGinArgMetProGiyAsnAlaMetValarg 135 	cent Similarity: 86.00 Matches: cent Similarity: 36.26% Conservative: t Local Similarity: 18.70% Mismatches: ry Match: 4.85% Indels:
Qy 136 GlyPheArgValalaTyrLySArgHisValLeuThrMetAspasp 150 	DB: US-09-848-852A-3 (1-332) x US-09-134-001C-1230 (1-2184)
151 LeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnAspGlnValMetAsnMetTyrGlyAsp	Qy 69 GluGluHisValThrCysValGlnSerIleLeuAspGluPheLeuGlnThrTyrGly 87
171	Qy 88 SerLeulleProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGln 107 :::

132	127	147	167 273	187 330	207	227 399	247	265	285 561	301	320		· · · · · · · · · · · · · · · · · · ·
TTGATTATTGTGAAT	GluPheSerThrProSerArgLysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArg :::	MetProGlyAsnAlaMetValArgGlyPheArgValAlaTyrLysArgHisValLeuThr         :::         :::         :::	MetaspaspleuGlyThrLeuTyrGlyGlnAsnTrpLeuasnaspGlnValmetasnMet :::::         :::         GatGaaaaTaGTGGTCATGCATGCGCGTAATATTGCATTAGAAGAAGTAGAAACCCT	TyrGlyAspLeuValMetAspThrValProGluLysValHisPhePheAsnSerPhePhe	TyraspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsnValAsp  :::    TTACAAAACTTTAAA	IlePheshrysGluLeuLeuLeulleFrolleHisLeuGluValHisTrpSerLeulle	SerValAspValArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArg        :::      TTGTTGATTTAGATCGAGTAAGGGTTGAATACTTTAATGCCAAAGAGAATATTAATTCA	ArgCysProLysHisIleAlaLysTyrLeuGlnAlaGluAlaValLysLysAsp	ArgleuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsn:::	AsnaspSeraspCysGlyAlaPheValLeuGlnTyrCysLysHisLeu	AlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgArgGln:::          :::      CGTATTTTAACTTCCCATTTATTTC	IleTyr 322   :::      GTCTAT 645	GENERAL INFORMATION:  GENERAL INFORMATION:  APPLICANT: RAKIZUKA, AKITA  APPLICANT: RAKIZUKA, AKITA  APPLICANT: RAKIZUKA, AKITA  TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph  TITLE OF INVENTION: Disease Gene and Uses Thereof  NUMBER OF SEQUENCES: 23  CORRESPONDENCE ADDRESS:  ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.  STREET: Two Militia Drive  CITY: Lexington  STATE: Massachusetts  COUNTRY: USA  COMPUTER: ERADABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC Compatible  OPERATING SYSTAM: PG-PASS-POSS  SOFTWARRE: PASPABLE FORM:  MEDIUM TYPE: IBM PC Compatible  OPERATING SYSTAM: PRIPARSE  SOFTWARRE: PASPABLE POSS/MS-DOSS  SOFTWARRE: PASPABLE POSS/MS-DO
118	108	128	148	168	188		228	248	520	286	302	321	RESULT 14 US-08-531-927B Sequence 8, Patent No. 5; PATELICANT TITLE OF TITL
QQ	Qy Db	Qy	Qy Db	Qy	Qy	Qy	Qy	Qy Dp	Qy Dp	Qy Db	Qy	Qy	RESCU US-SCU PS PS P

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283 TCAGGTTATAAGCAATGCCTTGAAAGTTTGGGGTTTAGAACTAATCCTGTTCAACAGTCC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 aTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLe 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 uPheSerThr-------ProSerArgLys----------115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 ----TyrGlnArgMet-----ProGlyAsnAlaMetValArgGlyPheArgValAl 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 TTATAAGGAACACTGGTTTACAGTTAGAAATTA------GGAAAACAGTGGTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 uAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysVa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 uAspGluPheLeuGln---ThrTyrGlySerLeuIleProLeuSerThrAspGluValVa 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 ACATCAGCTGGATGAGAGGAGGATGAGAATGGCAGAAGGAGGAGTACTAGGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::: ||||
223 TTATCGCACGTGTGACAGCAGCCTTCTGGAAATATGGATGACAGTGGTTTTTTCTCTAT
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45
24
53
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA: DP H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCYONEY/AGENT INHER: 32,227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
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US-08-902-622-1
; Sequence 1, Application US/08902632
; Generat No. 6008025
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                0.672
84.00
38.98%
25.42%
4.74%
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Best Local Similarity:
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---CTAGCGGAGAACAAGAGGATTCCC----- 3791
                                                                      APPLICANT: KAWAMURA, Yoshihisa
APPLICANT: TAKAGI, Masahiro
APPLICANT: TAKAGI, Masahiro
APPLICANT: THANNKA, Tadayuki
TITLE OF INVENTION: Modified Thermostable DNA Polymerase,
TITLE OF INVENTION: Amplification
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AlaSerIle------LeuIleSerAsnValCysSerIleGlyAspHisValAlaGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHisLeuAlaProProAsp 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 GluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLys 60
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                                                                                                                                                                                                                                                                                                                                                                                       3.50 inch floppy disk, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: hyperthermophilic archaeon STRAIN: KOD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: COCCUTENT HEREWITH CLASSIFICATION 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 198911/96
FILING DATE: 29-JUL-1996
APPLICATION NUMBER: JP 200446/96
APPLICATION NUMBER: JP 2015-1996
APPLICATION NUMBER: JP 2016-1996
ATTORNEY ASSON, Edward W. REGISTRATION NUMBER: 18,918
RECESTRATION NUMBER: 18,918
REFERENCE/DOCKET NUMBER: 2418/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-425-7200
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,632
FILING DATE: CONCURRENT HEREWITH
KOMATSUBARA, Hideyuki
                                                           KAWAKAMI, Bunsei
KAWAMURA, Yoshihisa
                                                                                                                                                                                                                                         ADDRESSEE: Kenyon & Kenyon
STREET: 1 Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-425-5288
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                      KAMIMURA, Hideki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 5342 base pairs
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31.90%
17.86%
4.74%
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EDNESS: double
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MEDIUM TYPE: 3.50 inc
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Best Local Similarity:
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STRANDEDNESS:
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Pred. No.:
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STATE:
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4038 GCCIACTACTCACACGTGATCCCCAAGGAAGTCCTGAGCGAGGTCTTTGGGAAGGTTTTC 4097
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1200 GTGCTCGACCGCGTTGACTCGTTGGAAGACTACGATGGTTATGTCTATGACCTG 4259
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                                                                                                                                                                                                                                                                                                  1918 CICGICCICCITCTIGAACICGGIGGGGICICTGCTGIAAAACITGGGCACGACAGCGGC 3977
                                                                                                                                                                                                                                                                                                                                                                                       4098 CAGAAAAACGTCAGTCCTCAGACCTTCAGGAAGATGGTCGAGGACGGAAGACTCGATCCC 4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4158 GAAAAGGCCCCAGAGGCTCTCCTGGCTC--------ATTGAGGGGGACGTA 4199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1320 TACTACGGTTACTACGGCTATGCAAGGGCGCGCTGGTAC-----TGCAAGGAGTGTGCA 4373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4374 GAGAGCGTAACGGCCTGGGGAAGGGAGTACATAACGATGACCATCAAGGAGATAGAGGAA 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4503 GAAACCGTCAAAAAGAAGGCTATGGAGTTCCTCAACTATATCAACGCCAAACTTCCGGGC 4562
                                                                                81 GluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValValGluLys 100
                                                                                                                                                                     101 LeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGlyLeuValLeuGln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------AsnTrpLeuAsnAspGlnValMetAsnMetTyrGlyAspLeu 171
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                                                                                                                  61 AlaGlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAsp
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OgvptO drosophila
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Ogm908 arabidopsis
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Og5k94 macaca fasc
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Og1879 arabidopsis
Og19795 drosophila

O9VWK5
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O05C2

311 282 307 266.5 266.5 266.5 253.5 253.5 253.5 253.5 253.5 253.5 201.5 193.5 113.5 113.5 113.5 113.5 113.5 113.5

Q94e62 oryza sativ Q91ss7 arabidopsis Q8w5n9 oryza sativ

Q94LG5 Q8W0H2 Q23238 Q94E62 Q9LSS7

**08RZ25** 

ALIGNMENTS

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88.726 Million cell updates/sec
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1772
1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_virus:\* sp\_vertebrate:\*

sp\_organelle:\*
sp\_phage:\*
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sp\_rodent:\*

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RESULT Q9Y3W9	LT 1 49
OI A	Q9x3w9 PRELIMINARY; PRT; 371 AA.
25	01-NOV-1999 (TrEMBLrel, 12, Created)
DŢ	(TrEMBLrel.
텀	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C	Hypothetical 42.2 kDa protein.
Z 0	HOME CASTALONS (Himman)
3 C	nomo saptens (numan). Rukarvota: Metazoa: Chordata: Craniata: Vertebrata: Ruteleostomi:
88	Primates;
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RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=UTERUS;
КX	
RA	Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA	Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA	
RA	Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA	Wambutt R., Korn B., Klein M., Poustka A.;
RT	"Towards a Catalog of Human Genes and Proteins: Sequencing and
RŢ	Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
RL	Genome Res. 11:422-435(2001).
DR.	EMBL; AL050283; CAB43384.1;
DR	HSSP; Q02724; IEUV.
DR	MEROPS; C48.003;
DR G	InterPro; IPR003653; SUMO_protease. pfsm: ps00000; psmtidses C/8. 1
4 :	Fram, Frosou, reputase_C40, 1.
SO	Hypothetical protein. SEQUENCE 371 AA; 42234 MW; EEE87C5885CA5082 CRC64;
no	94.18;
Ma	<pre>best Local Similarity 100.0%; Fred. No. 1./e-136; Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>
οy	19 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEABRPGEKAGQHSPLREEHVTCVQSI 78

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RQIYKELCHCKLTV
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                                                           VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ 258
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                                                  VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG
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                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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100.0%; Pred. No. 3.2e-136;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-20267842; PubMed-10806345;
Yeh E.T. Gong L., Kamitani T.;

"Ubiquitin-like proteins: new wines in Gene 248:1-14(2000).

EMBL: AXO08763; AAG33252.1; -.

HSSP; Q02724; IEUV.
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
Choi S.J., Jeon Y.J., Kim K.I., Nishimori S., Suzuki T., Uchida Shimbara N., Tanaka K., Chung C.H.;
Shimbara N., Tanaka K., Chung C.H.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF199459; AAL25652.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574 AA; 65009 MW; E495137EE7500741 CRC64;
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sentrin/SUNO-specific protease (SMT3 isopeptidase 1).
SMT31P1 OR SENP3 OR SMT31P.
                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1667; DB 4; 1
Pred. No. 3.2e-136;
                                                                                                                                                                                                   sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.1%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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Pfam; PF02902; Peptidase_C48; 1.
                                                                                                                                PRT;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
SUMO-1 specific protease 3.
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                                                                                                                                   PRELIMINARY;
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ROIYKELCHCKLTV 332
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Matches 314; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; C48.003;
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us-09-848-852a-3.rspt

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Pfam; PF02902; Peptidase_C48; 1.
                                                                                                         Best Local Similarity
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                                            SEQUENCE
                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8WP32;
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                                                                                                                                                                                                      Nishida T., Tanaka H., Yasuda H.;
"A novel mammalian Shri3-specific isopeptidase 1 (SMT3IP1) localized in the nucleolus at interphase."; care is second at interphase."; Eur. J. Biochem. 267:6423-6427 (2000).

EMBL: AXY08764; AAG33253.1; -.
EMBL: AXY08764; AAG38418.1; -.
HSSP: Q02724; IEUV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 568 AA; 6403 MW; 655F1FAB1AB62EA8 CRC64;
                                                                               Yeh E.T., Gong L., Kamitani T.;
"Ubiquitin-like proteins: new wines in new bottles.";
Gene 248:1-14(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Unknown (Protein for IMAGE:3448367) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.1%; Score 1637; DB 11; 98.1%; Pred. No. 1.3e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                     MEROPS; C48 003; --
MGD; MGI:2158736; Smt3ipl.
InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
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                                       STRAIN=C57BL/6J;
MEDLINE=20267842; PubMed=10806345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 308; Conservative
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                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                      PubMed=11029585;
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                                                                                                                                                                                                 117 LVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTV 176
                                                                                                                                                                                                                                                                                                             PEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFYDSQGIHFKFCVENIRKYLLTEAREKNRPEFLQGWQTAVTKCIPQQKNDSDCGVFVLQ 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 ISVDVRRRIITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN 286
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=TESTIS;
Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
Terao K., Sugano S.;
"Isolation of novel full-length cDNA clones from macaque testis cDNA
"lbraries.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 86.3 kDa protein
Hypothetical Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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                                                 Length 537;
                                                                                                               66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB074(NY 12) BAB72076.1; -.
InterPro; IPR003653; SUNO_protease.
Pfam; PF02902; Peptidase_C48; 1.
Hypothetical protein.
SEQUENCE 755 AA; 86290 MW; 40EC773CA29B8CEA CRC64;
537 AA; 61769 MW; 18F609C41D4B7DF9 CRC64;
                                                    44.5%; Score 789; DB 4;
54.0%; Pred. No. 5.1e-60;
iive 54; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.5%
Matches 152; Conservative
                                                                                                               Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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TISSUE-EMBRYO;
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351 SFYDSQGIHFKFCVENIRKYLLTEAREKNRPEFLQGWQTAVTKCIPQQKNDSDCGVFVLQ 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GEKAGQHSPLREEHVT-CVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 TYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQ 296
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 20.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang Y.-G., Li T.; "Identification of FKSG45, a novel gene located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
44.2%; Score 784; DB 4;
Best Local Similarity 53.6%; Pred. No. 1.1e-59;
Matches 147; Conservative 54; Mismatches 67;
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Pfam; PF02902; Peptidase_C48; 1.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 AELWIKELTSVYDSRARERLRQIEEQKALALQLQNQRLQER--EHSVHDSVELHLRVPLE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 EE-HVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQR 127
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                                                                                                                                                                                                                                                                                                                                                                                                                          19 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi Fujii A., Hara H., Nishikawa T., Nomira Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Mabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO00923; BAA9138.1;

SEQUENCE 191 AA, 20457 MW; B9F2B6F629F31612 CRC64;
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Gong L., Millas S., Maul G.G., Yeh E.T.H.;
"Differential Regulation of Sentrinized Proteins by
specific Protease.";
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sentrin/SUMO-specific protease.
                                                                                                                                                                                                                                                                                                   27.7%; Score 490; DB 4; I
100.0%; Pred. No. 1.1e-34;
Live 0; Mismatches 0;
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Best Local Similarity 34.0%; Pred. No. 5.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSR 191
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Pfam; PF02902; Peptidase_C48; 1.
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EMBL; AF149770; AAF31171.1; -.
HSSP; Q02724; 1EUV.
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Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 TLNRRCPKHIAKYLQAEAVKKDRLDFH-QGWKGYFKMN-VARQNNDSDCGAFVLQYCKHL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase.T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes.XVI. The complete sequences of 150 new cDNA clones from brain which code
                                          : | : | | | | | | : : | | : | | : | | : | | : | | : | | | | | : | : | : | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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Catarrhini; Hominidae; Homo.
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29.6%; Pred. No. 8.5e-26;
Live 64; Mismatches 107; Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
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Pfam; PF02902; Peptidase_C48; 1.
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DNA Res. 7:65-73(2000).
EMBL; ABG7752; BAA92569.1; -.
HSSP; Q02734; IEUY.
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
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nes 97; Conservative
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73 TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                        Euteleostomi;
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"Cloning of SENP2, a novel member of sentrin-specific protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 589;
                                                                                                                      Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF151697; AAG15309.2; -.
HSSP; Q02124; IEUV.
MEROPS; C48.007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
SEQUENCE 589 AA; 67890 MW; 75836FC41672E436 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DUN-2002 (TrEMBLrel. 21, Last annotation update) CDNA FLJ14693 fis, clone NT2RP2005360, weakly similar saplens sentrin/SUMO-specific protease (SENPI) mRNA.
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Last annotation update)
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                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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01-MAR-2001
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49 GMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQE 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 GQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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EMBL, RA508904, AAL14437.1; -. MEROPS, C48.007; -. MGD; MGJ:1923076; 4930538C18Rik.
                                                                                                                                                                                                                                           21.9%; Score 387.5; DB 11; Length 357; 32.0%; Pred. No. 2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 541;
                                                                                                                                                                           41001 MW; 9453B4A1989BD3BF CRC64;
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Last annotation update)
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31.4%; Pred. No. 5.6e-25;
Live 62; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 AA
                                                                                                                                                                                                                                                                                                                   54; Mismatches
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Mus musculus (Mouse).
                            MGD; MGI:2149738; 4930444G20Rik.
InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
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Pfam; PF02902; Peptidase_C48; 1.
SEQUENCE 541 AA; 62227 MW; 84AA
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                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                           357 AA;
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les 93; Conserv
       MEROPS; C48.010; -
                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 98; Conserv
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                                                                                                                                           NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                                                                                                                                                                                                                                                73 TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPKHIAKYLQAEAVKKDRLDF-----HQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLA 302
                                                                                                                                                                                                                                                                                                                                                                            SRRGYQLEP------GSNGLLRRK-- 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    561
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                            13 ARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505 ICEILLQYLQDESKTKRNSDLNLLEWTHHSMKPH---EIPQQLNGSDCGMFTCKYADYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 --VSIIETKEKNCSGKERDRRTDDLLELTEDM-EKEISNALGHGPQDEILSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 DKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 MVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
NCB[_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                           60;
                                                                                                                                                                           Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OL-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 17, Last sequence update)
Adult male testis cDNA, RIKEN full-length enriched library,
clone:4930444G20, full insert sequence (Fragment).
                                                                                                                                                                22.2%; Score 393; DB 4; Length 59
29.6%; Pred. No. 1.4e-25;
.ive 64; Mismatches 107; Indels
                                                                                                    444EDE041E96561F CRC64;
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562 RDKPITFTQHQMPLFRKKMVWEILHQQL 589
InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
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STRÁIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSQPFSFTQQDMPKLRRQIYKELCHCKL
                                                                                                    67952 MW;
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EMBL; AK015380; BAB29820.1;
                                                                                                                                                                                                                                           97; Conservative
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                                                                                                    590 AA;
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                                                                                                                                                                       Query Match
Best Local
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MEDLINE=2108560; PubMed=11217851;

A RAWAN J., Shihadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa J., Shihadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Rromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ry Sakin M.J., Bult C., Relecher C., Fujita M., Mombaerts P.,

Nordone P., Rang B., Ringwald M., Roofiyuez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Roofiyuez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyashaw-Boois A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nyasharisaki Y.
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                                                                                                                                     218 IHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFH-QGWKGY 276
                                                                                                                                                                                                                                                                                                           484
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                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                 DQVMNMYGDLVMDTVPEK - - - - VHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIP
                                                                                                                                                                                                                                                                                                                                                                            277 FKM--NVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL 330
                                                                                                                                                                                                                                                                                                                                                                                                                    SMKPHEIPQQLNGSDCGMFTCKYADXISRDKPITFTQHQMPLFRKKWVWEILHQQL 540
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Interpro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; L
SEQUENCE_S88 AA; 67579 MW; 09B56796Ca194847 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588 AA
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EMBL; AK015987; BAB30067.1; -.
HSSP; Q02724; 1EUV.
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Search completed: December 16, 2002, 20:11:15 Job time: 773 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2002, 19:26:20; Search time 167 Seconds Run on:

(without alignments)
33.125 Million cell updates/sec

US-09-848-852A-3

1772 1 MYSAQREWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105981 seqs, 16662342 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

Published\_Applications\_AA:

11: /cgn2\_6/ptodata/1/pubpaa/USOB\_NEW\_PUB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 3. Appli	· ~	ì	9	Sequence 13443, A	Sequence 34, Appl	Sequence 614, App	Sequence 200, App	Sequence 394, App	Sequence 16, Appl	Sequence 11364, A	Sequence 5222, Ap	Sequence 12143, A	Sequence 16, Appl	Sequence 46, Appl	Sequence 46, Appl	Sequence 15, Appl	Sequence 35, Appl	Sequence 1, Appli
	ID	US-09-848-852A-3	US-09-856-247A-2	US-10-008-461-2	US-09-815-242-13640	US-09-815-242-13443	US-09-866-582-34	US-09-925-302-614	US-09-765-272-200	US-09-801-368-394	US-09-890-813-16	US-09-815-242-11364	US-09-815-242-5222	US-09-815-242-12143	US-10-041-007-16	US-09-887-586A-46	US-09-903-012-46	US-10-041-007-15	US-09-866-582-35	US-10-007-706-1
	DB	10	10	12	10	10	10	10	10	10	9							6	10	6
	Query Match Length DB	332	621	212	427	427	824	304	674	803	439	865	638	642	782	782	782	817	820	1503
dР	Query Match	100.0	12.6	6.9	5.1	5.1	4.9	4.7	4.7	4.6	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4
	Score	1772	222.5	122.5	90.5	89.5	98	84	82.5	82	80	80	79	79	78.5	78.5	78.5	78.5	78.5	78.5
	Result No.		7	3	4	2	9	. 7	8	6	10	11	12	13	14	15	16	17	18	19

LENGTH: 332 amino acids TYPE: amino acid

SEQUENCE CHARACTERISTICS INFORMATION FOR SEQ ID NO: 3

Sequence 27, Appl Sequence 10886, A Sequence 11857, App Sequence 128, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 1152, A Sequence 1152, A Sequence 7, Appl Sequence 7, Appl Sequence 50, Appl Sequence 50, Appl Sequence 51, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 11036, A Sequence 1284, A Sequence 1884, A
US-09-905-173-27 US-09-815-242-4912 US-09-815-242-10686 US-09-870-759-128 US-09-815-242-11557 US-09-817-586A-24 US-09-815-242-11557 US-09-815-242-126 US-09-815-242-126 US-09-815-242-12 US-09-916-22 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-914-96-50 US-09-918-95-76-76-76-76-76-76-76-76-76-76-76-76-76-
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Tang, Y. Tom
Corley, Neil C.
Guegler, Rarl J.
Yue, Henry
Patterson, Chandra
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH EGF SIGNALING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/848,852A
FILING DATE: 07-May-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09848852A Patent No. US20020106373A1
                                                                                                                                                                                                                                                                                                STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
RESULT 1
US-09-848-852A-3
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us-09-848-852a-3.rapb

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Query Match
Best Local Similarity
Matches 47; Conserv
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| AHLILT || 617
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                211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09856247A
Patent No. US20020151028A1
GENERAL INFORMATION:
APPLICANT: Lima, Christopher
APPLICANT: Lima, Christopher
APPLICANT: Lima, Structure-Based Drug Design for Ulp1 Protease Substrates
FILE REFERENCE: 2650/16681-US1
CURRENT APPLICATION NUMBER: US/09/856,247A
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/205,336
PRIOR FILING DATE: 2000-05-18
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                                                                                                                                                                                                                                                                                                                                                                                             61 AGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQ 120
                                                                                                                                                                                                                                                                    61 AGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQOEFSTPSRKGLVLO 120
                                                                                                                                                                                                                                                                                                                  LIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKV 180
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                                                                                                                                                          Gaps
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                                                                                                                                                                                                      HFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFD
                                                                                                                                                                                      1 MYSAQRFWGTIWARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK
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0
                                                                                                                           Length 332;
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                                                                                                                                                         Indels
                                                                                                                        Query Match 100.0%; Score 1772; DB 10; Best Local Similarity 100.0%; Pred. No. 3.6e-167; Matches 332; Conservative 0; Mismatches 0;
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es 120;
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12.6%; Score 222.5; I
Best Local Similarity 25.2%; Pred. No. 6.5e
Matches 77; Conservative 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LALSQPFSFTQQDMPKLRRQIYKELCHCKLTV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-848-852A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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CLONE: 2056178
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                TOPOLOGY: 11
IMMEDIATE SOURCE:
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US-09-856-247A-2
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23.9%; Pred. No. 0.0001;
tive 32; Mismatches 75;
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TITLE OF INVENTION: New Protein
FILE REFERENCE: OGIO34(p80209)
CURRENT APPLICATION NUMBER: US/10/008,461
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 0027905.9
PRIOR PILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
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CURRENT APPLICATION NUMBER: US/09/815,242
KELLLIPIHL - EVHWSLISVDVRRRTITYFDS -
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10008461 Patent No. US20020127692A1 GENERAL INFORMATION:
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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CORGANISM: Homo sapiens
US-10-008-461-2
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20.5%; Pred. No. 0.51;
tive 52; Mismatches 114;
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APPLICANT: Rosenbaum, Joel L.
APPLICANT: Cole, Douglas G.
TITLE OF INVENTION: INTRAFLAGELLAR TRANSPORT
FILE REFERENCE: 07917-145001
CURRENT APPLICATION NUMBER: US, 60/206, 923
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13443
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Patent No. US20020127620A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pneumoniae US-09-815-242-13443
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APPLICANT: Apskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tanamoto, Robert T.
APPLICANT: Tanamoto, Robert T.
APPLICANT: An Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
FILE REPERENCE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASTESEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: PASTESEQ FOR WINDOWS VERSION 4.0
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; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13640
       2001-03-21
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APPLICANT: Haselbeck, Robert
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US-09-765-272-200
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (208)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
LOCATION: (229)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LSKLGELYDREGDKSQAFQYYYESYRYFPCNIEVIEWLG 627
                                                                                            242 QRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHL 301
                                                                                                                           --- ECLRFLVRLCTDL 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----RGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 RDNYTCPTEEEYKAMVLQKTGGLFGLAVGLMQLFSDYKEDLKPLLNTLGLFFQIRDDYAN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHIAKYLQAEAVKKDRLD-----FHQGW---KGYFKMNVARQNNDSDCGAFVLQYCKH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 MDTVPEKVHFFNSFFY---DKLRTKGY-DGVKRWTKNVDIFNKELLLIPIH----LEVHW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 SFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITY---FDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | || : || 56 VTEMLHNASLLIDDIEDNSKLRRGFPVAH-----SIYG------SIYG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 114;
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US/00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PAtentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7%; Score 84; DB 10; Length 304; 18.7%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Mismatches
                                                                                                                                                                              ALSQPFSFTQ-----QDMPKLRRQIYK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LALSQPFSFTQQDMPKLRRQIYKEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 YLEDVGSFEYTRNTLKELEAKAYKQI 279
                                                                                                                                                                                                                                                                        Sequence 614, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 YQRMPGNAMV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 61; Conserv
                                                                                                                        677 YKDTHRKFPENV
581 VIPTDPQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER
SOFTWARE: Pater
SEQ ID NO 614
                                                                                                                                                                                                                                          RESULT 7
US-09-925-302-614
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                                                                APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 ESEGMFYFHILGDSYYEKVYDNVŚIFENLYET------QEMKSFALISAWGK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 AYKRHVLTM--DDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 LYKARLFEQLRFDIGKLGEDGYLNQKVY-----LLSEKVIYLNKSLYAYRIRKG-- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 GVKR-WTKN-----VDIFNKELLLI-----PI--HLEVHWSLISVDVRR------RTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 EAERPGEKAGQHSPLRE---EHVTCVQS---ILDEFLQT-YGSLIPLSTDEVV---
                                                                                                                                                                                                                                                                                             COMPUTER FEADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7%; Score 82.5; DB 10; 22.1%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79;
                                                                                                                                                                Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-0an-2001
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: «Unknown>
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 200:
US-09-765-272-200
                                                                                                                                                                                 STREET: 9410 Key West Avenue
Sequence 200, Application US/09765272 Patent No. US20020061545A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 394, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 674 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ'ID NO: 200 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Conservative
                                                                                                                                                                                                         CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 YFD---SQRTLNR 247
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18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 TDEVVEKL---EDIFQQEFSTPSRK-GLVLQLIQSYQR-MPGNAM--VRGFR-----VA 140
                                                                                                                                                                                                                                                                    141 YKRHVLTMDDLGT-LYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTK---- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                   195 -GYDGVKRWTKNVDIFNKEL-----LLIPIHLEVHWSLISV--DVRRRTITYFDSQR 243
                                                                                                                                                                                      157 GSDL----TATTIGKALG----LREIQVWKDVDGVLTCDPNI-----YANAVPVPYLT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 KAGQHSPLREEHVTCVOSILDEFLQTYGSLIPLS----TDEVVEKLEDIFQQEFSTPSR 114
                                                                                                Gaps
                                                                                                                                           45 GSDLGMAEEAERPGEKAGQHSPLREEHV----TCVQSILDEFLQTYGSLIP---LS 93
                                                                                                                                                                                                                                                                                                                                                                                   262 LKSNITMLDIVSTRMLGQYGFLAKVFSIFEDLGISV-------DSVATSEVSIS
                                                                                             88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CASELDECK, KODELL
APPLICANT: CASKING, JUGITH W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tradit, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/10,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR PELLING DATE: 2000-12-26
PRIOR PELLING DATE: 2001-02-16
PRIOR PELLING DATE: 2001-02-16
PRIOR PELLING DATE: 2001-02-16
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                                                Length 439;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 TLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSD 289
                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.5%; Score 80; DB 10; Best Local Similarity 23.7%; Pred. No. 12; Matches 36; Conservative 27; Mismatches 51
                                             4.5%; Score 80; DB 9;
21.0%; Pred. No. 4.6;
iive 52; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11364, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                Conservative
                                                                    Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-815-242-11364
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US-09-815-242-11364
US-09-890-813-16
                                                Query Match
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                                                                                                                                                                                                                                                     APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Slumers, Infet
APPLICANT: Summers, Eiff
APPLICANT: Summers, Eiff
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.14
CURRENT APPLICATION NUMBER: US 09/487,558
PRIOR PILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER: US 60/160,587
NIORE FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NOS: 440
SEQ ID NO 394
LENGTH: 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 MVSKGDYDGOKNGKAKKIRSOLLKNPPETTSLINDVQNLLNSISKDYEN----ETVQXNE 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :: :|| :: | :: | :| SKLLEAESKEQIMEQIRNQLPAEKIQSMLPPTVLLKARINAY------KRNDKHLTNV 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 HVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDT-VPEKVHFFNSFFYDKLRTKGYDGVKRW 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 TKNVDIFNKELLLIPIHLEVHWSLI-----SVDVRRRTITYFDSQRTLNRRCPKHIAKY 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLEDIF-----QQEFSTPSRKGL--VLQLIQSYQRMPGNAM------VRGFRVAYKR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 LGIIADESS---GIDWDSSE-----YDADEPFKVEFLSDFLEDKLQ-KNYEG--DI 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 MAEEAERPGEKAGQHSPLREE------HVTCVQSILDEFLQTYGSLIPLSTDEVVE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 803;
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Publication No. US20020183486A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: Aspartate Kinase
FILE REFERENCE: BB1430 PCT
CURRENT APPLICATION NUMBER: US/09/890,813
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/172944
PRIOR APPLICATION NUMBER: 60/172944
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Mccrosoft Office 97
SEQ ID NO 16
LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 4.6%; Score 82; DB 10;
Local Similarity 22.2%; Pred. No. 6.8;
nes 56; Conservative 41; Mismatches 95,
                                                                                                                                                                                   No. US20020128250Alman, Thea
Royer, John
Salama, Sofie
Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Triticum aestivum
                                                                 Hecht, Peter
Holtzman, Doug
Madden, Kevin
                    APPLICANT: Busby, Robert APPLICANT: Cali, Brian
                                                                                                                                           Maxon, Mary
Milne, Todd
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Best Local S
Matches 56
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---IQQRDLYYQKRMQEYESQQAEIKRLETFVEKNITRASTSGMAKSRRKILEKMERID 307
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APPLICANT: Xu, H Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DEORARY OLS
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2010-12-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 12143
LENGTH: 642
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18.7%; Pred. No. 9.9;
tive 49; Mismatches
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; Sequence 12143, Application US/09815242
; Patent No. US20020061569A1
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US-10-041-007-16
Sequence 16, Application US/10041007
Patent No. US20020144736A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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Zyskind, Judith W.
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Matches 56; Conservative
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APPLICANT: Haselbeck
APPLICANT: Ohlsen,
APPLICANT: Zyskind,
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   653 KAFDHQNLSEEELLGLKNILKEDFNAHVSLEDLKKASPIENFVAEKLKSDYENK----- 706
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                                                                           115 KGLVLQLIQSYQRMPGNAMVRGFRVAY------KRHVLTMDDLGT---LYGQNWLNDQ
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APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: W. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1000-103-21
PRIOR REPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22-16
PRIOR PILING DATE: 2001-22-16
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4.5%; Score 79; DB 1
Best Local Similarity 18.7%; Pred. No. 9.8;
Matches 56; Conservative 49; Mismatches
                                                                                                                                                                                                                                 164 V-----MNMYGDLVMDTVPEKVHFFNSFFYD 189
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5222, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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LENGTH: 638
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                    APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
FILE REFERENCE: P02081US1
CURRENT APPLICATION NUMBER: US/10/041,007
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Indels
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US-09-887-586A-46
Sequence 46. Application US/09887586A
Sequence 46. Application US/09887586A
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094556All, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR PILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR PILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR PELING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 46
SEQ ID NO 46
SEQ ID NO 46
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.4%; Score 78.5; D
Best Local Similarity 23.4%; Pred. No. 15;
Matches 40; Conservative 32; Mismatches
APPLICANT: Matsuda, Seiichi P.T.
                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Ables grandis
US-10-041-007-16
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600 EDYLLGYYEEAEWLAAEYVPTLDE----YIKNGITSIGQRILLLSGVLIMD 646
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Search completed: December 16, 2002, 19:39:09 Job time : 168 secs

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3, Appli
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4067, Ap
56, Appl
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Sequence 5
Sequence 7
Sequence 7
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Sequence 5
Patent No.
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6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-375-709-3
US-08-134-001C-4067
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US-09-134-001C-562-30
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21; expression AERPGEKAGQH-----SPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLED 103 RGF----RVAYKRHV-----LTMDDLGTLYGQ--NWLNDQV-MNMYGDLVM 173 DTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVD-IFNKELLLIPIHLEVHWSLISVDVR 232 104 IFQQEFST------PSRKGLVLQLIQSYQRMPG--------NAMV 134 1 MYS----AQRFWGTIWARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLG----MAEE 53 GENERAL INFORMATION:

APPLICANT: Calgene, LLC
TITLE OF INVENTION: Production of polyunsaturated fatty acids by expring TITLE OF INVENTION: Production of polyunsaturated fatty acids by expring INVENTION: Of polyketide-like synthesis genes in plants; FILE REFERENCE: CGNE.131.01US
CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT APPLICATION NUMBER: 60/048,650
EARLIER FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 654 221 AYQYGATLGKHDHGIVDAALGKGLSKGEITYVAP--DYTLNSEGKWETLT----IDGLEM Sequence Seq Sednence Sed DB 4; Length 654; Indels 5.2%; Score 91.5; DB 4; llarity 21.2%; Pred. No. 0.5; Conservative 43; Mismatches 118; US-09-360-545-16 US-09-384-393-46 US-09-234-393-13 US-09-234-393-40 US-09-234-393-40 US-09-865-171-13 US-09-865-171-38 US-09-865-171-40 US-09-865-171-40 US-09-865-171-40 US-09-865-171-40 US-09-171A-27 US-08-646-27 US-09-412-184-27 US-09-412-184-27 US-09-412-184-27 US-08-465-28 Sequence 2, Application US/09090793 Patent No. 6140486 Shewanella putrefaciens Best Local Similarity Matches 78; Conserv RESULT 1 US-09-090-793-2 ; ORGANISM: SI US-09-090-793-2 78.5 778.5 778.5 778.5 778.5 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 778.7 7 TYPE: PRT Query Match 54 135 ð g δ р ŏ g Q g ò

281 VARQNNDS 288

RRTITYFDSQRTLNRRCP--KHIAKYLQ-----AEAVKKDRLDFHQGWKGYF-----KMN

233 394

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for Eicosapentaenoic Acid Synthesizing
Process for Production of Eiscosapentaenoic
336 NAFGQDVEVLFASHSAPVWGNQAINDFLRLQRDNYGLVHNQTLRLANDGVGIQDIGDAIQ 395
                                               174 DTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVD-IFNKELLLIPIHLEVHWSLISVDVR 232
                                                                                                                                          233 RRIITYFDSQRTLNRRCP--KHIAKYLQ-----AEAVKKDRLDFHQGWKGYF----KMN 280
                                                                                                                                                                           Gaps
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                                                                              COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,929
FILING DATE: 20-NOY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-7AN-1995
PRIOR APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-WAY-1993
FILING DATE: 14-WAY-1993
FILING DATE: 15-WAY-1993
APPLICATION NUMBER: UP 4-147945
FILING DATE: 15-WAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAMADA, Akiko
APPLICANT: KATO, Seishi
APPLICANT: KATO, Seishi
TITLE OF INVENTION: Gene Coding fo
TITLE OF INVENTION: Enzymes and Pr
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08752929
Patent No. 5798259
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202)672-5300
(202)672-5399
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amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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// MOLECULE TYPE: protein
US-08-752-929-3
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                                                                                                                                                                                                                                                                                             484 MAEPENDS 491
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STATE: D.C
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US-08-752-929-3
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APPLICANT: YAMADA, Akiko
APPLICANT: KATO, Seishi
APPLICANT: KATO, Seishi
APPLICANT: KANDO, Kiyosi
TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of
TITLE OF INVENTION: Eiscosapentaenoic Acid
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 IXSHSHADHFGGA-----RGVQEMFPDVKVYGS-----DNITKEIVDENVLAGNAMSRRA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AYQYGATLGKHDHGIVDAALGKGLSKGEITYVAP--DYTLNSEGKWETLT----IDGLEM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AERPGEKAGQH-----SPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 RGF----RVAYKRHV------LITMDDLGTLYGQ--NWLNDQV-MNMYGDLVM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.2%; Score 91.5; DB 1; Length 661;
Best Local Similarity 21.2%; Pred. No. 0.51;
Matches 78; Conservative 43; Mismatches 118; Indels 129; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MYS---AQRFWGTIWARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLG----MAEE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 IFQQEFST-----PSRKGLVLQLIQSYQRMPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/150/AAOK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
APPLICATION DATE:
APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,709
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
                                                                                                                    US-08-375-709-3; Sequence 3, Application US/08375709; Patent No. 5683898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202)672-5300
(202)672-5399
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LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WEGNER, Harold C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-375-709-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                             GENERAL INFORMATION:
     :| || || 482 MAEPENDS 489
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Sequence 3242, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCTITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .026 --IHVIINAKFNVEPSLVDTALLQIELNSMLQSLPKQLTKRKIVNPKSQKDIQV----- 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED TITLE OF INVENTION: THEREON NUMBER OF SEQUENCES: 62 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 VDIFNKE-----LLLIPIH--LEVHWSLISVDVRRRTITYFDSQ------RTLNRR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 CPKHI---AKY-LQAEAVKKDRLDFHQGW-----KGYFKMNVARQNNDSDCGAFVLQYC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 VEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGN--AMVRGF-----RVAYKRHVLTMDD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVK-----RWTKN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.7%; Score 83; DB 4; Best Local Similarity 22.4%; Pred. No. 10; Matches 59; Conservative 46; Mismatches 94
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PELICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56, Application US/08180209B Patent No. 5593877 GENERAL INFORMATION:
APPLICANT: King, Te-Piao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1078 -HIA-NOTLELLODDLNSLRROL 1098
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  RIFNFPFYF -----RGEVY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hackensack
                                                                     RESULT 5
US-09-134-001C-3242
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3242
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CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-14

RIOR FILING DATE: 1997-08-14

RIOR FILING DATE: 1997-08-14

RUMBER OF SEQ ID NOS: 5674

LENGTH: 727
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                                                                                                                   135 RGF----RVAYKRHV------LTMDDLGTLYGQ--NWLNDQV-MNMYGDLVM 173
                                                                                                                                                                                                                                                                                                       | | : | | | | | 336 NAFGQDVEVLFASHSAPVWGNQAINDFLRLQRDNYGLVHNQTLRLANDGVGIQDIGDAIQ 395
                                                                                                                                                                                                                                                                                                                                                                      DIVPEKVHFFNSFFYDKLRIKGYDGVKRWTKNVD-IFNKELLLIPIHLEVHWSLISVDVR 232
                                                                                                                                                                                                                                                                                                                                                                                                                    427
                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 RRTITYFDSQRTLNRRCP--KHIAKYLQ-----AEAVKKDRLDFHQGWKGYF-----KMN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCPKHIAKYL--QAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHL---- 301
                                           173 IYSHSHADHFGGA----RGVQEMFPDVKVYGS-----DNITKEIVDENVLAGNAMSRRA 222
                                                                                                                                                                                    ----NAMV 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 AERPGEKAGQH-----SPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 YDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNR
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1 MYS---AQRFWGTIWARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLG--
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4.9%; Score 86; DB 4; Length 727;
Best Local Similarity 18.7%; Pred. No. 2.3;
Matches 49; Conservative 46; Mismatches 93; Indels
                                                                                                                                                                                    --PSRKGLVLQLIQSYQRMPG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ALSQPFSFTQQDMPKLRRQIY 322
                                                                                                                                                                               104 IFQQEFST-----
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GENERAL INFORMATION:
APPLICANT: Te Piao KING
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
TITLE OF INVENTION: CLONING AND PROPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
TITLE OF INVENTION: THERAPIES BASED THEREON
FILE REFERENCE: 2313/0F138US
CURRENT APPLICATION NUMBER: US/09/166,205B
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 ----GDLV------MDTVPEKVHFFNSFFYDKLRTKGYDGV-----KRWTKNVDIFNK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 KDPNGNVVARNGGVPQLGNLTKHLQVFRDHLINQIPDKSFPGVGVIDFESWR------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELLLIPIHLEVHWS-----LISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 -LFMEETLKAAKRMRPA----ANWGYYAYPYCYNLTPNQPSAQCEATTMQENDKM 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.7%; Score 82.5; DB 4;
Best Local Similarity 19.5%; Pred. No. 1.7;
Matches 46; Conservative 43; Mismatches 70;
                                                                                                                                                                                                                             600-1-074 CIPB
                     APPLICATION NUMBER: US 08/180,209
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATE: US 08/031,400
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                                                                                                                 FILING DATE: 11-MAR-1993
ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26/742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
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US-09-166-205B-56
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US-08-474-853-56
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LENGTH: 343
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TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPF----SFTQQDMPKL 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.7%; Score 82.5; DB 1; Length 343; 19.5%; Pred. No. 1.7; tive 43; Mismatches 70; Indels 7
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APPLICATION NUBER: US/08/474,853
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 CIP
TELECOMUNICATION INFORMATION:
TELEPAX: 201 487-5800
TELEFAX: 201 343-1684
ITELEX: 133521
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                  APPLICATION NUMBER: US/08/180,209B
FILING DATE: 11-7An-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56, Application US/08474853
Patent No. 6287559
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 46; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-08-180-209B-56
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212 ELLLIPIHLEVHWS-----LISVDVRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKD 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 FGLGLERLAMILYDIPDI-RLFWCEDERFLKQFCVSNINQKVKFQPLSKYPAVINDISFW 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 ELF----QGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIP-LSTD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 200, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                  162 -LEMEETLKAAKRMRPA-----ANWGYYAYPYCYNLTPNQPSAQCEATTMQENDKM 211
                                                                                                                                      266 RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPF----SFTQQDMPKL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 451;
                                                                             64 KDPNGNVVARNGGVPQLGNLTKHLQVFRDHLINQIPDKSFPGVGVIDFESWR-
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APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Oroxco, Buddy
APPLICANT: Schwaber, James S.
FILE REFERENCE: BB-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
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; Pred. No. 2.6;
46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 60/093,530
EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 FRVAYKRHVLTMDDLGTLYGQNWLND-----
                                                                                                                                                                                                                                                        US-09-357-251-35
; Sequence 35, Application US/09357251
; Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Office 97
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.7%
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-961-083-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-357-251-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: F
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: King, Te-Piao
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                              ELLLIPIHLEVHWS-----LISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKD 265
                                                                                                                     -----PIFRQ-NWASLQPYKKLSVEVVRREHPFWDDQR-VEQEAKRREKYGQ------ 161
                ----GDLV------ADTVPEKVHFFNSFFYDKLRTKGYDGV-----KRWTKNVDIFNK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 ----GDLV------MDTVPEKVHFFNSFFYDKLRTKGYDGV-----KRWTKNVDIFNK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | || || || : :: || || || || || 4 NKTVREFNVYMNVPTFMCHKYGLRFEEVSEKYGILQNWMDKFRGEEIAILYDPGMFPALL 63
                                                                                                                                                                          266 RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPF----SFTQQDMPKL 317
                                                                                                                                                                                                     77;
                                                    64 KDPNGNVVARNGGVPQLGNLTKHLQVFRDHLINQIPDKSFPGVGVIDFESWR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 NAMVRGFRVAYK-----RHVLTMDDLGTLYG--QNWLN----DQVMNMY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.7%; Score 82.5; DB 5; 19.5%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600-1-074 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: PCT/US94/02629
10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/180,209
FILING DATE: 11.7AN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/031,400 FILING DATE: 11-MAR-1993 ATTONEY/AGENT INFORMATION: NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                     Sequence 56, Application PC/TUS9402629 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 13353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: · IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
NO
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ADDRESSEE: Klauber &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: Sil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07601
                                                                                                                                                                                                                                                                                                  PCT-US94-02629-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US94~02629-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                  116
              169
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99 EKLEDIFQQEFSTPSRKGL-VLQLIQSY----QRMPGNAMVRGFRVAYKRHVLTMDDLGT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 LYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKEL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 SDLGMAEEAERPGEKAGQHSPL-----REEHVTCVQSILDEFLQTYGSLIPLSTDEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BESS, Jannetje W.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: VERSER, Christiaan
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 LLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 353;
                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/034,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.8%; Prec. ....
                                                                                                                                                                                                                                                                                                     NAME: KGKULIS, Paul N. REGISFREATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELECOMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.6%; Score 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN, DARBY & CUSHMAN
TYEET: 1615 L. Street, N.W.
CITY: WASHINGTON
                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2IP: 20036-5601
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08449015 Patent No. 5804409
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                           TELEPAN: (202) 861-300
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 353 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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20036-5601
                                                                                                                                                                     FILING DATE:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EKLED----IFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 ESEGMFYFHILGDSYYEKVYDNVSIFENLYET------QEMKSFALISAWGK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AYKRHVLTM--DDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 LYKARLFEQLRFDIGKLGEDGYLNQKVY------LLSEKVIYLNKSLYAYRIRKG-- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 GVKR-WTKN-----VDIFNKELLLI-----PI--HLEVHWSLISVDVRR------RTIT 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08034650
Patent No. 5641671
GENERAL INFORMATION:
APPLICANT: BOS, Jannetje W.
APPLICANT: FRENKEN, Leon G.
APPLICANT: VISSEN, Cornelis T.
APPLICANT: PRODUCTION. OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 EAERPGEKAGQHSPLRE---EHVTCVQS---ILDEFLQT-YGSLIPLSTDEVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 674;
                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCIL Text CURREMY APPLICATION DATA: APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.7%; Score 82.5; Di
Best Local Similarity 22.1%; Pred. No. 4.9;
Matches 56; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: CUSHMAN, DARBY & CUSHMAN: 1615 L. Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                               NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEFAN: (301) 309-8504
TELEFAN: (301) 309-851
INFORMATION FOR SEQ ID NO: 200:
                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 674 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
  ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-961-083-200
                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : || ||:
259 YKEFEMKQRLLNQ 271
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US-08-034-650-11
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NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFRENCE/DOCKET NUMBER: A-587
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 19.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 KGYFKMNVARQNNDSDC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSILOMNGCHIXNFNXC 285
                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                      ; LOCATION: 1..500
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-117-083-68
                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-041-991A-10
                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | : | : | : | | : 1129 RR-EIAAQLDGSPAQAEALGVWRRYRAYFDALAQLPGDGAVLGDKLDPAAMQLALDQRAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 LYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKEL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 EKLEDIFQQEFSTPSRKGL-VLQLIQSY----QRMPGNAMVRGFRVAYKRHVLTMDDLGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDLGMAEEAERPGEKAGQHSPL····REEHVTCVQSILDEFLQTYGSLIPLSTDEVV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 68, Application US/08117083
Patent No. 5719054
GENERAL INFORMATION:
APPLICANT: Boursnell, Michael E. APPLICANT: Inqlis, Stephen C. APPLICANT: Munro, Alan J. TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 LLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 353;
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  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                          NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPANS: (202) 82-0944
TELEX: 6714627 CUSH
INFORMATION FOR EQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.6%; Score 82; DB 1
Best Local Similarity 20.8%; Pred. No. 2;
Matches 48; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Walter H. Dreger
4 Embarcadero Center, Suite 3400
                                 APPLICATION NUMBER: US/08/449,015
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                  CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: protein US-08-449-015-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Walter H
STREET: 4 Embarcade:
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                amino acid
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SOFTWARE:
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64 YMKTMGSCIQMDSMEALEYLSELKESGGWSPRPEMQEFEYPDGVEDTESIERLVEEFFNR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 VLCISVRRKRTSSTRVDSSRYINLGMRLPRHTCALSKWKDAVVLCLQIGQNHGIMILMVS 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 FLQTYGSLIPLSTDEVVEKLEDIFQ------QEFSTP-----SRKGLVLQLIQS 124
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the open reading frame."
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Batent No. 6107278

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....r Pes
STREET: Saliwanchik, Iloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; Score 81.5;
19.8%; Pred. No. 4;
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COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILING DATE: 13-MAR-1998
A-58783
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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                             24 ASILISNVCS-IGDHVAQEL----FQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                             Query Match
4.6%; Score 81.5; DB 3; Length 633;
Best Local Similarity 23.2%; Pred. No. 5.7;
Matches 52; Conservative 33; Mismatches 96; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 AFRGLNTRIHDMLEFRTYMFLNVFEYVSIWS----LFKYQSLLV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 KVHFFNSFFYDKLRTKGY-----DGVKRWTKNVDIFNKELLLI 216
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERROKE/DOCKET NUMBER: MA-709
TELECOMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPAX: (352) 375-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
STROPOLGS: linear
MOLECULE TYPE: peptide
US-09-041-991A-10
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Search completed: December 16, 2002, 19:28:42 Job time : 39 secs

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December 16, 2002, 19:28:00 ; Search time 899 Seconds (without alignments) 49.209 Million cell updates/sec
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2: /SIDSZ/gcddta/geneseqp-embl/AA1981.DAT:*
4: /SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*
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8: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
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11: /SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
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17: /SIDSZ/gcgdata/geneseqy-embl/AA1991.DAT:*
18: /SIDSZ/gcgdata/geneseqy-embl/AA1995.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                   1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                   US-09-848-852A-3
1772
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111:
12:
13:
14:
15:
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                                                                                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human fetal brain	Human polypeptide	Human polypeptide	Human polypeptide	Amino acid sequenc	Human polypeptide	Human ovarian anti	Human protein sequ	Human polypeptide	Human protein sequ
SUMMARIES			ID		AAM39269	AAM41055	AAM41056	AAB31977	AAM39270	ABP41139	AAM25617	AAO04440	AAB92493
			DB	21	22	22	22	22	22	23	22	22	22
			re Match Length DB I	371	371	438	438	568	354	309	270	119	191
	dР	Query	Match	94.1	94.1	94.1	94.1	94.1	88.0	83.0	44.1	34.7	27.7
			Score	1667	1667	1667	1667	1667	1558.5	1470	781.5	614.5	490
		Result	NO.		7	m	4	5	9	7	80	σ	10

s cra a s	Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human EST product Arabidopsis ESD4 ( Rice EST product Herbicofally activ A. thaliana enviro	Drosophila melanog Human gene 11 enco Drosophila melanog Human secreted pro Human SUMO-1 SEQ I Human polypeptide Novel human diagno Human protein sequ	Human secretory po Human protein phos Novel human diapos Gene 4 human secre Drosophila melanog Lactococcus lactis Human protein SEQ Lactococcus lactis Lactococcus lactis Lactococcus lactis
197 197 197 197 197 197 197	AAC45770 AAC45772 AAC25055 AAC25056 AAW8618 AAW86185 AAW86185 AAW8033	ABB64875 AAE01755 AAE01755 AAY91646 AAG78297 AAG78297 AAG14039 AAB94888	ABB97801 ABB04392 AAB34354 ABB63890 ABB53442 ABB53442 ABB54137 ABB54137
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## Human fetal brain cDNA clone vb7\_1 derived protein #1. A AAY50911 standard; Protein; 371 (first entry) 10-MAR-2000 AAY50911; AAY 50911

ALIGNMENTS

Human; secreted protein; treatment; nutritional activity; cytokine; cell proliferation; cell differentiation; hematopoiesis regulation; tissue growth; activin; inhibin; chemotactic; chemokinetic; hemostatic; thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;

980S-0088994. 980S-0089278. 980S-0091647. 980S-0097639. 99WO-US08504 98US-0082904 (ALPH-) ALPHAGENE INC 11-JUN-1998; 12-JUN-1998; 02-JUL-1998; 24-AUG-1998; 22-APR-1999; Homo sapiens. W09955721-A1 23-APR-1999; gene therapy 24-APR-1998; 04-NOV-1999 

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amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
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Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 AA;
                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253,
N-PSDB; AAI58425
                                                                            WO200153312-A1
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                     Homo sapiens.
                                                                                                                              26-DEC-2000;
                                                                                                                                                        21-JAN-2000;
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Wang J, Y
Zhao QA,
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                                                                                                                                      This invention describes novel human secreted proteins which are encoded by polynucleotides obtained from fetal brain, adult skin, adult brain, adult them. Adult thymus and adult acrta cDNA libraries. The polynucleotides and perdicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hemostatic stimulating activity, tissue growth activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, adherin/tumor inhibition activity. The polynucleotides are also stated to be useful for gene therapy.

ANY50905-X50947 represent the secreted proteins described in the method of the invention which are encoded by the polynucleotides represented in
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                                                              New polynucleotides encoding secreted human proteins, derived from human fetal brain, adult skin, adult brain, adult heart, adult thymus and adult aorta cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
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  Rapiejko P;
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100.0%; Pred. No. 7e-157;
ive 0; Mismatches 0;
 Hall J,
                                                                                                                 Claim 21a; Page 223-225; 282pp; English.
 Hoffman H,
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  Yuan
                         WPI; 2000-052801/04
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                                      N-PSDB; AAZ43782
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 Valenzuela D,
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's parkinson's disease, unutington's disease, and contral nervous system suppression of the activities such as: Immune system suppression, activity, chemoteatic/chemokinetic activity, hemoteatic/chemokinetic activity, hemoteatic/chemokinetic activity, hemoteatic/chemokinetic activity, hemoteatic/chemokinetic activity, and streaming assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAYKRHVLIMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 237
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chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating disorders
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Zhang J;
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Yang Y,
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100.0%; Pred. No. 7e-157;
ive 0; Mismatches 0;
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u C, Xue AJ,
Drmanac RT;
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such as central nervous system injuries
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Wehrman T, Xu C,
Goodrich R, Drman
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317
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Matches 314; Conservative
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W0200153312-A1.
specification.
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14-SEP-2000;
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09-JUL-2000;
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Wang J, 1
Zhao QA,
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Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, the encoded polypeptides (AAM8642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system as peripheral nervous system along as and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy Drager Synfonme. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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         259 AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR 318
                      Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for treating disorders
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Zhang J;
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Yang Y,
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iu C, Xue AJ,
Drmanac RT;
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Wehrman T, Xu C,
Goodrich R, Drman
                                                                                                                                    AAM41055 standard; Protein; 438 AA
                                                                                                                                                                                                        Human polypeptide SEQ ID NO 5986.
                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0488725.
2000US-0552317.
2000US-0598042.
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Wang Z,
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Zhao QA,
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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305 VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ 364
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                                                                                                                                       19 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR
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                                         Length 438;
                                                                                           Indels
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Yang Y,
                                         94.1%; Score 1667; DB 22;
100.0%; Pred. No. 8.9e-157;
ive 0; Mismatches 0;
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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2000US-055317.
2000US-0598042.
2000US-065312.
2000US-0653450.
2000US-0653450.
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                                                                  Best Local Similarity 100.
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 RQIYKELCHCKLTV 438
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438 AA;
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WO200109292-A2.
                           08-FEB-2001
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                                                                                                                                Gong L,
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                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic asaft thrombolytic activity, arthritis and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 198
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; de-sentrinase; SENP; SENP1; SENP2; SENP3; chromosome 12q13.1; sentrin-specific profease; sentrin; anti-proliferative agent; anti-viral agent; herpes slmplex-1; cytomegalovirus; sentrinisation; PML; tumour suppressor; acutte promyelocytic leukaemia.
                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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                                                                                                                                                                                                                                                                                                                                                          Length 438;
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                                                                                                                                                                                                                                                                                                                                                       94.1%; Score 1667; DB 22;
100.0%; Pred. No. 8.9e-157;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a human SENP3 polypeptide.
                                                                             Example 2; SEQ ID NO 5987; 10078pp; English.
                                                   system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB31977 standard; Protein; 568 AA.
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                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100. Matches 314; Conservative
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 WPI; 2001-442253/47
                                                                                                                                                                                                                                                                                                                               438 AA;
            N-PSDB; AAI60212
                                                                                                                                                                                                                                                                                                      specification.
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The present sequence represents human de-sentrinase (SENP) 3 polypeptide. The specification describes SENP1 and SENP2 polypeptides. The SENP1 gene is found in chromosome 12q13.1. SENP1 is found in the nucleus, SENP3 is found in the nucleus, and SENP3 is found in both locations. SENP3 is found in both locations. SENP3 is found in both locations. SENP3 polypeptides are sentron-specific proteases that remove sentrin from some sentrinised peptides, but do not affect proteins anodified by ubiquitin or NEDD8. SENP polypeptides are used to identify specific modulators of SENP. These modulators are potential anti-proliferative and anti-viral agents such as herpes simplex-1 or cytomeqalovitus. SENP polypeptides are used for studying the role of sentrinisation in the biological function of PML, a tumour suppressor implicated in development of acute promyelocytic leukaemia. Fragments of SENP colynucleotides are used as hybridisation probes and amplification primers for detecting gene expression or preparing mutated sequences, also as antisense sequences for inhibiting SENP expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding de-sentrinase polypeptides, useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1667; DB 22;
Pred. No. 1.3e-156;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 1121-122; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                 antiproliferative or antiviral agents
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100.0%; Pre
                                                           99US-0146774
31-JUL-2000; 2000WO-US20884
                                                                                                                   (TEXA ) UNIV TEXAS SYSTEM.
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Matches 314; Conserva
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                                                           31-JUL-1999;
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VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 198
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ABP41139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification.
                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humthington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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Yang Y,
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Pred. No. 3.9e-146;
0; Mismatches .0;
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Xue AJ,
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Wang Z, Wehrman T, Xu C,
Zhou P, Goodrich R, Drman
                                Human polypeptide SEQ ID NO 2415.
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94.6%;
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2000US-0552317.
2000US-0598042.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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 (first entry)
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Matches 297; Conservative
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                                                                                                                                                                        Homo sapiens.
22-OCT-2001
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14-SEP-2000;
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                                                                                                                                         leukaemia.
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Zhao QA,
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to CDNAs encoding them (ABQ54131-ABQ556305), and also encompasses polypeptides 90% identical and polynuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; infection; informatory condition; immune disorder; blood disorder;
                                         237
                                                                                                                                                                                                                                                                                                              AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR 318
                                                                                                                                                                                                                                                                                                                                                                 cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ovarian antigen HOFOB27, SEQ ID NO:2271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID No 2271; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP41139 standard; Protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2001; 2001WO-US18569.
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22-DEC-2000; 2000WO-US35017.

WO200153455-A2

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disorders, infections (e.g., chiammydia, HTV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired toxoplasmosis, and toxic vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may deneraby, chromosome mapping, in the condition of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present esquence represents a human ovarian antigen of the invention.

Concertification but was obtained in electronic form at directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

antinfilammatory; antirheumatic; antiarthritic; immunosuppressive;

A mitiantial endocrine; cardiant; central nervous system; virucide;

anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

A dermatologicide; antimutagen; cardiovascular; antianaemic; inceremic

A dermatological; antiallergic; antiasthmatic; cortectaric;

A munostimulant; gene therapy; antisense therapy; vaccine; inflammation;

A mitianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

A cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

A enetic disease; haematopoietic disorder; platelet disorder; asthma;

A llergic rhinitis; diabetes; multiple sclerosis; depression;

A larbeimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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  polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 FSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 GMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLIS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 VDVRRRITIYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1470; DB 23; Length 309;
Pred. No. 2e-137;
0; Mismatches 8; Indels 0,
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                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein sequence SEQ ID NO:1132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM25617 standard; Protein; 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.0%;
97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      309 AA;
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AAM25963. The proteins can have activities based on the tissues and calls they are expressed in, such as: antinichamatory; antirheumatic; calls they are expressed in, such as: antinichamatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiants; cardiansculf; antianaemic; antiagregant; hadmostafic; vulnerary; cardiavascular; antianaemic; antiagregant; hadmostafic; uninerary; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; cardiabetic; cytostatic; neuroprotective; antidepressant; nootropic; cording them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity genetic diseases, hadmatopoietic disorders, canaemia, platelet disorders, thrombocytopsenia, wounds, burns, ulcers, cateoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, cardiacal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GEKAGQHSPLREEHVT-CVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 LVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 PDKVHFFNSFFHRQLVTKGYNGVKRWTKKVDLFKKSLLLIPIHLEVHWSLITVTLSNRII 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFYDSQGIHFKFCVENIRKYLLTEAREKNRLNL-QGWQTAVTKCIPQQKNDSDCGVFVLQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment and diagnosis of e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 235; 1217pp; English.
                                                                                                                                                  99US-0471275.
2000US-0488725.
2000US-0552317.
                                                                                                                                                                                                                                                                                         Tang YT, Liu C, Drmanac RT;
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Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                  WPI; 2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 AA;
                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH99558
                                                                                                                                                                           21-JAN-2000;
25-APR-2000;
                                                                                                                                                      23-DEC-1999;
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RESULT 9

Homo sapiens

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AAB92493 standard; Protein; 191 AA.
                                                                                                                26-JUN-2001
    AAB92493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 GYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 KYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDM 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.7%; Score 614.5; DB
85.2%; Pred. No. 5e-53;
live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                     AA004440 standard; Protein; 119 AA.
                                                                                                                                                        Human polypeptide SEQ ID NO 18332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                           WO200164835-A2.
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                           06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders
                                                                 AAO04440;
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AA004440
                                                               A PART OF THE PROPERTY OF THE 
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of a noligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs are present human cDNA sequences; AAH13628 and AAH13628 co AAH13628 co AAH13629 condition than amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human mino acid sequences; and AAH13629 to AAH13632 represent human mino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.7%; Score 490; DB 22; 100.0%; Pred. No. 2.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 10591; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
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Human protein sequence SEQ ID NO:10591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-2000;
                                                                                                                                                                                                                                SP1074617-A2
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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79 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSR 114

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RESULT 10

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439 NQDEVLSEAFRL----TITRKDIQTLNHLNWLNDEIINFYMNMLMERSKEKGLPSVHAF 493
                                                                                                                                                                                                                                AAB31976 standard; Protein; 509 AA
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                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.2;
Best Local Similarity 29.6;
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                   15-MAY-2001
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                                                                                                                                                                                                                                                          AAB31976;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human de-sentrinase (SENP) 1 polypeptide. The specification describes SENP2 and SENP3 polypeptides. The SENP1 gene is found in rhomosome 12q13.1. SENP1 is found in the nucleolus, and SENP3 is found in the nucleolus, and SENP3 is found in both locations. SENP polypeptides are sentron-specific proteases that remove sentrin from some sentrinised peptides, but do not affect proteins modified by ubiquitin or NEDD8. SENP polypeptides are used to identify specific modulators of SENP. These modulators are potential anti-proliferative and anti-viral agents such as herpes simplex-1 or cytomegalovirus. SENP polypeptides are used for studying the role of sentrinisation in the biological function of PML, a tumour suppressor implicated in development of acute promyelocytic leukaemia. Fragments of SENP polymerofices are used as hybridisation probes and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 AELWIKELTSVYDSRARERLRQIEEQKALALQLQNQRLQER--EHSVHDSVELHLRVPLE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EE-HVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 MPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primers for detecting gene expression or preparing mutated sequences, also as antisense sequences for inhibiting SENP expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                         de-sentrinase; SENP; SENP1; SENP2; SENP3; chromosome 12q13.1;
                                                                                                                                                                                                    sentrin-specific protease; sentrin; anti-proliferative agent; anti-viral agent; herpes simplex-1; cytomegalovirus; sentrinisation; PML; tumour suppressor; acute promyelocytic leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 ASILISNVCSIGDHVAQE----LFQGSDLGMAEEAERPGEKAGQHS------PLR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding de-sentrinase polypeptides, useful as antiproliferative or antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a human SENP1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 456; DB 22;
Pred. No. 3.2e-36;
 156 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSR 191
                                                                                 Ā.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 2; 122pp; English.
                                                                              AAB31973 standard; Protein; 643
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34.0%;
                                                                                                                                                                                                                                                                                                                                        31-JUL-2000; 2000WO-US20884
                                                                                                                                                                                                                                                                                                                                                                  99US-0146774
                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       ETH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF54827
                                                                                                                                                                                                                                                                                   WO200109292-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Yeh
                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                   15-MAY-2001
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                                                                                                          AAB31973;
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                                                                                                                                                                     301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; de-sentrinase; SENP; SENP1; SENP2; SENP3; chromosome 12q13.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sentrin-specific protease; sentrin; anti-proliferative agent; anti-viral agent; herpes simplex-1; cytomegalovirus; sentrinisation; PML; tumour suppressor; acute promyelocytic leukaemia.
                                         244 TLNRRCPKHIAKYLQAEAVKKDRLDFH-QGWKGYFKMN-VARQNNDSDCGAFVLQYCKHL
                                                                                                                                                                                                                       NSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
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29.6%; Pred. No. 4.2e-30;
.ive 64; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                        302 ALSQPFSFTQQDMPKLRRQIYKELCHCKL 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani H;
Midorikawa Y;
                                                                                  188
                                                                                                     363
                                                                                                                                           423
                                                                                                                                                                       424 ICEIILLQYLQDESKTKRNSDLNLLEWTHHSMKPH---EIPQQLNGSDCGMFTCKYADYIS 480
                                            TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blood tests
       13 ARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHV
                  263 --VSIIETKEKNCSGKERDRRIDDLLELTEDM-EKEISNALGHGPQDEILSS-----
                                                                                133 MVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFY
                                                                                                                       DKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRKTITYFDSQRTLNRR
                                                                                                                                                            CPKHIAKYLQAEAVKKDRLDF-----HQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLA
                                                                                                                                                                                                                                                                                                                                              Human; stomach cancer; marker; screening; micro-metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stomach cancer-associated genes, useful as markers in screening for the early stages of the disease \cdot
                                                                                                                                                                                                                                                                                                                            Human stomach cancer expressed polypeptide SEQ ID NO 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 167-169; 242pp; Japanese
                                                                                                                                                                                                 303 LSQPFSFTQQDMPKLRRQIYKELCHCKL 330
                                                                                                                                                                                                              A.
                                                                                                                                                                                                                                                                   AAM94011 standard; Protein; 589
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99JP-0300253.
99US-0159590.
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17-FEB-2000; 2000US-0183322.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                         peritoneal dissemination.
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                         231 SRRGYQLEP-
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                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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18-OCT-1999;
                                                                                                                                                                                                                                                                                                         13-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                              38-FEB-2001
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Kodama T,
                                                                                                                                                                                                                                                                                      AAM94011;
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189 DKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRR 248
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                                                                                                                                                                                                                                                             311 SRRGYOLEP-----GILSEEVSARLRLGS-------GSNGLLRRK-- 342
                                                                                                                                                                                                                                                                                                          TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
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                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; diagnosis; antisense therapy; gene therapy,
                                                                                                                                                                                                                                                                                                                                      | : | : | : | : : | 343 --VSIIETKEKNCSGKERDRRTDDLLELTEDM-EKEISNALGHGPQDEILSS-----
                                                                                                                                                                                                                                                                                                                                                                                            133 MVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFY
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screening for compounds to treat the disease. They can also predicting micro-metastases. The gene can predict peritoneal
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                                                                                                                                                                        90;
                                                                                                                               Length 589;
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito K,
Otsuki
                                                                                                                    ; Score 393; DB 22;
; Pred. No. 5.2e-30;
64; Mismatches 107;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID NO:17423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 LSQPFSFTQQDMPKLRRQIYKELCHCKL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB95254 standard; Protein; 589
                                                                                                                             22.2%;
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27-A0G-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0241899.
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                                                                                                      Query Match
Best Local Similarity 29.00.
Local Similarity 29.00.
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                                                                                  589 AA;
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                                             dissemination.
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                                                                                      Sequence
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Myers EW;

Li PWD,

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2000US-191637P. 2000US-0614150.

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23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC, Adams M,
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11-JUL-2000;
               27-SEP-2001
               NAME OF COLOR OF STREET OF
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                                                                                                                            The present invention describes primer sets for synthesising your comprises: (a) an oligo-dT primer and an oligonucleotide complementary comprises: (a) an oligo-dT primer and an oligonucleotide complementary comprises of the 5602 nucleotide squences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide comprises a 1'-end sequence complementary to a polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers and encoded by the MAH13633 to AAH13633 to AAH13633 to AAH13632 to AAH13633 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.2%; Score 393; DB 22; Length 589; 29.6%; Pred. No. 5.2e-30; live 64; Mismatches 107; Indels 66
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Claim 8; SEQ ID 17423; 2537pp + CD ROM; English
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561 RDKPITFTQHQMPLFRKKMVWEILHOOL 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB59432 standard; Protein; 468 AA.
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WO200171042-A2.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical furge. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||: ||:||:||: ||: ||: || ||: ||: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 SIFKPKKQFDTSDFVIESVQNIPRQLDGSDCGIFSCMFAEYITCDVPITFTQSEMLYFRK 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 MDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK-----VHFFNSFFYDKLRTKGYDGVKR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 LIPL-TEEHHDRFNEITQDDKST----------EIIFKFNLHIT 277
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                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 5088; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 468;
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28.5%; Pred. No. 5.2e-22;
tive 55; Mismatches 85
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Matches 70; Conservative
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KMALEI 463
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Title: Perfect score:

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Sequence 17. Applisequence 223, Applsequence 223, Applsequence 38, Applsequence 19, Applsequence 117, Applsequence 1139, Applsequence 14, Applsequence 14, Applsequence 177, Applsequence 177, Applsequence 25, Applsequence 177, Applsequence 25, Applsequence 25, Applsequence 25, Applsequence 25, Applsequence 23, Applsequence 23, Applsequence 177, Applsequence 177, Applsequence 177, Applsequence 177, Applsequence 177, Applsequence 178, Applsequence 178, Applsequence 178, Applsequence 178, Applsequence 259, Applsequence 254, Applsequ
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Sequence 14, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 13, Appl
Sequence 11, Appl
                            Sequence 74, Appl
Sequence 7902, Ap
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang, Y. Tom
Corley, Neil C.
Guegler, Karl J.
Yue, Henry
Patterson, Chandra
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH EGF SIGNALING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
Comports: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
NRT APPLICATION DATA:
RAPLICATION NUMBER: US/09/848,852A
FILING DATE: 07-May-2001
0. US-09-867-701-4735
0. US-09-960-253-74
0. US-09-960-253-74
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US-09-903-012-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pharmaceuticals,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09848852A Patent No. US20020106373A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Ph
STREET: 3174 Porter
     COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
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-0=/Cgn2_1/USPTO_spool/US09848852/runat_16122002_132039_19075/app_query.fasta_1.519
-0=/Cgn2_1/USPTO_spool/US09848852/runat_16122002_132039_19075/app_query.fasta_1.519
-0B=Published_Applications.Na - OFMT=fastap - SUFFIXTA-npb - MINAMICH=0.1
-LOOPEXI=0 - LOOPEXI=0 - UNITS=blts - START=1 - END--1 - MATRIX=blosum62
-TRANS-human40.cdi - LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100
-THR_MIN=0 - ALIGN=15 - MODE-LOCAL - OUTFMT=pto - NORM=ext - HEAPSIZE=500 - MINEN-0
-MAXLEN=200000000 - USER-US09848852_CGGN_11-49_cfunat_16122002_132039_19075
-NCPU-6 - ICPU-3 - NO_XLPXY - NO_MMAP - LARGEQUERY - NEG_SCORES=0 - WAIT - LONGLOG
-DEV_IIMEOUT=120 - WARN_IIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELOFEXT=7
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1710, Ap
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Sequence 835, App
Sequence 1710, Ap
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                                                                                                                                                                          2002, 20:11:20 ; Search time 98 Seconds (without alignments) 1339.725 Million cell updates/sec
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1 MYSAQRFWGTINARRGAHLA......DMPKLRRQIYKELCHCKLTV 332
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| cgn2_6/ptodata/J/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/J/pubpna/PUB_NE_PUB.seq:*
| cgn2_6/ptodata/J/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/J/pubpna/USO6_PUBCOMB.seq:*
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| cgn2_6/ptodata/J/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/J/pubpna/USO8_NEW_PUB.seq:*
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| cgn2_6/ptodata/J/pubpna/USO9_NEW_PUB.seq:*
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| cgn2_6/ptodata/J/pubpna/USO0_NEW_PUB.seq:*
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| cgn2_6/ptodata/J/pubpna/USO0_NEW_PUB.seq:*
| cgn2_6/ptodata/J/pubpna/USO0_PUBCOMB.seq:*
                            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-983-965-835
US-09-777-564-1710
US-09-856-247A-1
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Matches:
Conservative:
Mismatches:
Indels:
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                    ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

RECISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0515 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEPRAX: 650-845-4166

INFORMATION FOR SEO ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1991 base pairs
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       APPLICATION NUMBER: 09/069,725 FILING DATE: <Unknown>
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                                                                                                                   TYPE: nucleic acid STRANDEDNESS: single
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PRIOR APPLICATION DATA
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Best Local Similarity:
                                                                                                                                                         LIBRARY:
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US-09-983-965-835/c

Sequence 335, Application US/09983965

Sequence 335, Application US/09983965

Setent No. US200201371601

GENERAL INFORMATION:

APPLICANT: Tao, Nengbing

APPLICANT: Byact, John C.

APPLICANT: Byact, John C.

APPLICANT: Byact, John C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 37-21(1029)

CURRENT FILING DATE: 2001-10-26

PRIOR PAPLICATION NUMBER: US 09/465,231

PRIOR APPLICATION NUMBER: US 09/465,231

PRIOR PLING DATE: 1999-12-15

PRIOR FILING DATE: 1999-12-15

PRIOR FILING DATE: 1999-12-17

NUMBER OF SED ID NOS: 5912

SEQ ID NOS: 5912
                                                                                                                            ValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHis 300
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                                                                                                                                                                                                                                                                                                   28 IleSerAsnValCysSerIleGlyAspHisValAlaGlnGluLeuPheGlnGlySerAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: 29-LIB188-017-Q1-E1-H1
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ORGANISM: Bos taurus
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                                                                            GluPheSerThrProSerArgLysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArg 127
                                                                                                                       MetProGlyAsnAlaMetValArgGlyPheArgValAlaTyrLysArgHisValLeuThr 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCAGC 194
                                                                                                                                            72
ValArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysPro
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                                 SerLeuIleProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGln
                                                                                                                                                                                                                               Sequence 1710, Application US/09777564

Batent No. US200202591A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Marmion, Jane
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493

CURRENT APPLICATION NUMBER: US/09/777,564

CURRENT FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 1730

SOFTWARE: FastSEQ for Window Version 4.0
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ORGANISM: Homo sapiens
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US-09-777-564-1710/c
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LENGTH: 503
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APPLICANT: Lima, Christopher
APPLICANT: Mossessova, Elena
APPLICANT: Mossessova, Elena
TITLE OF INVENTION: Structure-Based Drug Design for Ulp1 Protease Substrates
FILE REFERENCE: 2650/16681-US1
CURRENT APPLICATION NUMBER: US/09/856,247A
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 60/205,336
PRIOR APPLICATION NUMBER: 60/205,336
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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              LysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetVal 134
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311 GlnGlnAspMetProLysLeuArgArgGlnIleTyrLysGluLeuCysHisCysLysLeu
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                 Sequence 1, Application US/09856247A Patent No. US20020151028A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Saccharomyces cerevisiae
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222.50
43.46%
25.16%
12.56%
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                                                           ThrVal 332
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                                                                                                                                      US-09-856-247A-1
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                    1681 GGAGAAGACTTT------GATTTGATTCATTTAGATTGTCCGCAGCAACCA 1725
                                                                                                                                                                                                                                  266 ArgLeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsn 285
                                                                                                                                                                                                                      AsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHisLeuAlaLeuSerGln 305
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                                                                      AspValArgArgArgThrIleThrTyrPheAspSer------GlnArgThrLeu
                                                                                                                     246 AsnArgArgCysProLysHisIleAlaLysTyrLeuGlnAlaGluAlaValLysLysAsp
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4735, Application US/09867701
Patent No. US20020132237a1
GENERAL INFORMATION:
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEC ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches:
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57.14%
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Best Local Similarity:
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Sequence 7902, Application US/09878574

Patent No. U520020110548A1

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE OF INVENTION: U15401)B
CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2172 AAATCATGAAACAACTAATCTGTCAATACAGCAAAAACGGCATGGGAGGTAAAAACATG 2231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2232 GACCCGGCACGTAGATATTTTGAGAAGGATTTTTATTTTTGTACCCCTTAATGAAGCTGC 2291
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APPLICANT: Benson, Darin R.
APPLICANT: Monamath, Raodoh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.556
CURRENT FILIANG DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
SOFTWARE: FastSEQ for Windows Version 4.0
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Conservative:
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                                                               US-09-960-253-74
; Sequence 74, Application US/09960253
; Patent No. US20020123619A1
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53.70%
31.48%
8.13%
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US-09-960-253-74
425 AAGGAGCTG 433
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US-09-878-574-7902
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LENGTH: 5540
TYPE: DNA
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159 TrpLeuAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGlu 178
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16 TIGAGTTACATGGACACTACTGCGGCCAATCAGATGTCTCACTATTGGATCCGCCAAGC 75
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
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Batent No. US20020127692a1

GENERAL INFORMATION:

APPLICANT: Barbara ink

APPLICANT: Barbara ink

APPLICANT: Alan Lewis

TITLE OF INVENTION: New Protein

FILE REFREENCE: QC1034(p80209)

CURRENT APPLICATION NUMBER: US/10/008,461

CURRENT FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: 0027905.9

PRIOR FILING DATE: 2000-11-15

WHIGHER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0
                                                                        ORGANISM: Glycine max
COTHER INFORMATION: Clone ID: 701100484H1
US-09-878-574-7902
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122.50
40.40%
24.24%
6.91%
PRIOR FILING DATE: 1999-06-14
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130.50
52.50%
33.75%
7.36%
             NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 7902
LENGTH: 264
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(636)
US-10-008-461-1
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                              TYPE: DNA
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Patent No. US20020102543A1

GENERAL INPORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Annals
TITLE OF INVENTION: No. US20020102543A1e1 Mutated Mammalian Cells and
TITLE OF INVENTION: Annals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION UNMBRE: US/09/728,445
CURRENT APPLICATION NUMBRE: US 60/168,358

PRIOR FILING DATE: 1999-12-01
                                                                         223 CTTGAACCACTGGACCTCCCCAAGAGAGTTGTATTTTTAGCCATCAATGATAACTCC
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Mismatches:
Indels:
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                                                    179 LysValHisPhePheAsnSerPhePheTyrAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
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115.50
84.85%
66.67%
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US-09-728-445-223
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Best Local Similarity:
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LENGTH: 100
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267 LeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsnAsn 286
                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                           APPLICANT: Lalqudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: 4pril 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOUTWARE: PERL PROGram
SEQ ID NO 3098
LENGTH: 263
TUNDE TO SURVENTION NO SU
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Betent No. US20020072595A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PARTICK J. Dillon et al.
TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands
FILE REPERENCE: PB324D1
CURRENT APPLICATION NUMBER: US/09/956,004
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 08/976,259
PRIOR PLICHION DAMER: 60/061,953
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-10-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAACTCAITGAATGCGATAAAATATTTGTCCCTGTGCATAAAAGATGTACATTGGTGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 IleSerValAspValArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsnAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700347190H1
US-09-294-093B-3098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-848-852A-3 (1-332) x US-09-294-093B-3098 (1-263)
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Mismatches:
Indels:
200 LysArgTrpThrLysAsnValAspIlePheAsnLysGlu 212
                                 Length:
Matches:
                                                                                                                                                        Sequence 3098, Application US/09294093B
Patent No. US20010051335Al
GENERAL INFORMATION:
APPLICANT:
Lalqudi, Radhunath V
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110.00
47.068
24.718
6.218
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
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US-09-956-004-58
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1350 CTATITICCCTCGCTCGCCTAGGTATTGTGACGATGTTCGAACAACGACTTTGGTGAAT 1409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 LeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArg 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 ValAlaTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------AspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrVal 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 LeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLysAla 61
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59
31
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                         Length:
PRIOR APPLICATION NUMBER: 60/031,626
PRIOR FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 4835
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                                                                                                                                                                                                                                                                                                              108.00
31.69%
20.77%
6.09%
                                                                                                                                                                                ; ORGANISM: Escherichia coli
US-09-956-004-58
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Best Local Similarity:
Query Match:
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TYPE: DNA
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                                                                                                                                                                  FEATURE:
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APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.201
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILLING DATE: 2000-02-15
------GlyTyrAspGlyValLysArgTr 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 ArgHisVal-LeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnAs 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 oGluLysValHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLys-----
                                                                                                                                        Sequence 19, Application US/09924401

Patent No. US20020142957A1

GENERAL INFORMATION:

APPLICANT: Hepler, William T.

APPLICANT: Jiang, Yuqiu

APPLICANT: Vu, Jiangchun

TITLE OF INVENTION: AND DIANGOSIS OF COLON CANCER

FILE REPERENCE: 210121.550

CURRENT APPLICATION NUMBER: US/09/924,401

CURRENT FILING DATE: 2001-08-07

NUMBER OF SEQ ID NOS: 85

SEQ ID NO 19

LENGHA 577
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30
21
24
22
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7988, Application US/09783590 Patent No. US20020110850A1 GENERAL INFORMATION: APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.00034
103.00
53.128
31.258
5.818
                                                                              1971 GATGAAGAGTGC 1982
                                              287 AspSerAspCys 290
                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-924-401-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-783-590-7988
                                                                                                                              US-09-924-401-19/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR PAPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PAtentIn Ver. 2.0
SOFTWARE: PAtentIn Ver. 4.72
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NAME/KEY: misc feature
LOCATION: (184)
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NAME/KEY: misc feature
LOCATION: (263)
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NAME/KEY: misc feature
LOCATION: (308)
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NAME/KEY: misc feature
LOCATION: (375)
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NAME/KEY: misc feature
LOCATION: (406)
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (283)
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LOCATION: (226)
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LOCATION: (323)
OTHER INFORMATION: n eq
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LOCATION: (354)
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LOCATION: (240)
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LOCATION: (330)
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LOCATION: (387)
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LOCATION: (396)
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Alignment Scores:
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (449)
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LOCATION: (437)
OTHER INFORMATION: n equals a,t,g, or NAME/REY: misc feature
LOCATION: (439)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (452)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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US-09-925-302-171
IS-09-925-302-171
Sequence 171, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
                                                                                                                                      LOCATION: (442)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (427)
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CIHER INFORMATION: n equals a, t, g, US-09-783-590-7988
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584 CTCCATCAGGGACAAGGCTAGATATTACTGGAGGGATAATTACACTTGTCCCACTGAA
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## APPLICANT: Rosen et al.
### TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
### FILE REFERENCE: PAIO4
### CURRENT APPLICATION NUMBER: US/09/925,302
### CURRENT FILING DATE: 2001-08-10
### PRIOR PILING DATE: 2001-03-08
### PRIOR PILING DATE: 2000-03-08
### PRIOR PILING DATE: 1999-03-12
### NUMBER OF SEQ ID NOS: 896
### SEQ ID NOS: 896
### SEQ ID NO SEQ ID NOS: 820
### SEQ ID NOS: 820
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Indels:
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CORGANISM: Homo sapiens
US-09-925-302-171
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Best Local Similarity:
Query Match:
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764 CTCTTTTCCAAATTAGGGATGATTATGCTAATCTACACTCCAAAGAATATAGTGAAAAC 823
                                                  --LeuAspPh
                                                                                         AAAAGTTTKTGTGAAGATCTGACAGAGGAAAAGTTCTCATTCCTACTATTCATGCTATT
                                                                                                                                       eHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsnAsnAspSerAs
                                                                                                                                                                                                                                                                                                                                                                    994 ATACACTCGTAATACCCTTAAAGAGCTTGAAGCTAAAAGCCTATAAACAGATT 1045
                                                                                                                                                                                                                                                                                                                       308 rPheThrGlnGlnAspMetProLysLeuArgArgGlnIleTyrLysGluLeu 325
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APPLICANT: Oblsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Tarwick, John D.
APPLICANT: Tarwick, John D.
APPLICANT: Tarmanco, Robert T.
APPLICANT: Tarmanco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION UNMBER: 06/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/223,625
PRIOR PELING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-848-852A-3 (1-332) x US-09-815-242-9542 (1-1284)
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Matches:
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Mismatches:
Indels:
Gaps:
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PRIOR FILING DATE: 2000-12-22
PRIOR PPLICATION NUMBER: 60,269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9542
LENGTH: 1284
                                             256 rLeuGlnAlaGluAlaValLysLysAspArg--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9542, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Streptococcus pneumoniae
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US-09-815-242-9542
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Best Local Similarity:
Query Match:
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498
                                                                                                                                                                                                                                                                                                                                                                                                         177 ProGluLysValHisPhePheAsnSerPhePheTyrAspLys------LeuArg 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ThrLysGlyTyrAspGlyValLysArgTrpThrLysAsnValAspIlePheAsnLysGlu 212
                                                        534
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| S35 GGAAGTGAGGAGTCCATTTCCCAAATCAATCTAACTAATTTGCAAGAAAATTTTACAAAG 594
                                                                                                                                                                     GluAspilePheGln------GluGluPheSerThrProSerArgLys 115
                                                                                                                                                                                                                             130 GlyAsnAlaMet---valArgGlyPheArgVal-------AlaTyrLySArg 143
                                                                                                                                                                                                                                                                                                                                                HisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnAspGln 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 ValMetAsnMetTyrGlyAspLeuValMetAspThr----------------Val 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               889 TTTCAAAAATGTTATGAATCAGGTAAAATTGATGCATCCTTATCTTGTAGGAAGTTGAAGTA 948
                            61
                                                                                     81
                            LeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLysAla
                                                                                     GlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAspGlu
                                                                                                                                               PheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValGluLysLeu
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163 CCAGATTCGTGTTTATTCTTTTCAACTTTAGCGAAT
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 16, 2002, 19:36:15; Search time 257 Seconds

(without alignments)
124.189 Million cell updates/sec

Title:
Berfect score: 1772
Sequence: 1772
Sequence: 1772
Sequence: 1772
Sequence: 1772
Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 200000000
Maximum DB seq length: 200000000
Post-processing: Minimum Match 100%
Listing first 45 summaries
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1: pir1:\*
2: pir2:\*
4: pir4:\*
4: pir4:\*
Score Greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR\_73:\*

Database :

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T39840

conserved hypothetical protein SPBC19G7.09 - fission yeast (Schizosaccharomyces pombe C; Specias: Schizosaccharomyces pombe C; Specias: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999 C; Accession: T39840

RESULT 2

oligopeptide ABC t 90K protein - alfa transposase of ISI hypothetical prote hypothetical prote probable isoleucin transposase of ISI DNA topoisomerase hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable 3-oxoacyl hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote	ALIGNMENTS 586K0919.1 - human on 11-Jun-1999 #text_change 13-Aug-1999 .W.; Gassenhuber, J.; Wiemann, S. tabase, March 1999	tch  41.18; Score 1667; DB 2; Length 371;  42.18; Score 1667; DB 2; Length 371;  43.14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  43.14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  43.14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  43.14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  43.14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  44.16; Interpretation 0; Interpretation 0; Gaps 0;  45.16; Interpretation 0; Interpretation 0; Gaps 0;  46.16; Interpretation 0; Interpretation 0; Gaps 0;  47.16; Interpretation 0; Interpretation 0; Gaps 0;  48.16; Interpretation 0; Interpretation 0; Interpretation 0; Gaps 0;  48.16; Interpretation 0; Gaps 0; Gaps 0; Gaps 0;  49.16; Interpretation 0; Gaps 0;
G72420 WMFM9 1086671 102621 F86386 B81982 E80738 A84470 E83881 A43381 A43381 A43381 A43381 A7301 C70231	ALIGNMEN n DKFZp586K0919 -revision 11-Ju ewes, H.W.; Gas ence Database, 0283 uterus; clone D	Score ; Pred. 0; Mis ELFQGSDL [
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625 790 273 1201 1201 1472 1472 1472 1198 1198 11173 11173 11173	protein DKFZp s (man) equence_revisi , D.; Mewes, H in Sequence Da 6471 SL:ALO50283 adult uterus;	94.  1arity 100  Conservative 100  Conservative 111111111111111111111111111111111111
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97 97 97 97 97 97 97 97 97 97 97 97 97 9	1 hypot 13: Hono 13: Hono 10: To 10:	DKFZp58 Match Local Siles 314; Local LAPPD 19 LAPPD 58 LAPPD 79 LDEFL 111 LDEFL 79 VAYKR 19 VAYKR 111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111   111
0 11 22 24 24 24 24 24 24 24 24 24 24 24 24	RESULT 1 T08759 conserved hypothetical protein DKFZp; C;Species: Homo sapiens (man) C;Date: 11-Jun-1999 #sequence_revisic C;Accession: T08759 R;Wambutt, R.; Heubner, D.; Mewes, H submitted to the Protein Sequence Dai A;Reference number: 216471 A;Accession: T08759 A;Molecule type: mRNA A;Residues: 1.371 <	A, Note: D  Query M Best Lo Best Lo Atches  Qy 139  Qy 139  Qy 139  Qy 259  Qy 259  Qy 259  Qy 259  Db 298  Qy 319

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hypothetical protein F6N23.7 - Arabidopsis thaliana (protein F6N23.7 - Arabidopsis thaliana (protein F6N23.7 - Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C;Accession: T01233
R;Geisel, C
R;Geisel, C
R;Description: The EMBL Data Library, April 1998
R;Accession: T01233
R;Reference number: 214281
R;Ref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National protein YPL020c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein LPB11c
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Jaccesion: S63462
R.Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; Submitted to the EMBL Data Library, September 1995
A; Reference number: S63462
A; Reference number: S63462
A; Residues type: DNA
A; Coss. references: BMBL: U36624; NID: g1276642; PID: g1039457; GSPDB: GN00016; MIPS: YPL0
C; Genetics:
A; Cross-references: SGD: S005941
A; Map position: 16L
                                                                                                                                                                                                                     98 SRWTTKRKLGYDLIDCDIIFVPIHIDIHWTLGVINNRERKFVYLDSLFT-----GAK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 KRWTK----NVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAK 255
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                                                                                                                                                                               -- DTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDV
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A;Introns: 9/1; 21/2; 52/3; 85/3; 115/3; 147/3; 182/2; 213/3
                                                                                                                                                                                                                                                                                                                                                        : | ::|| | ::|| | 397 GEKKIEFYDSLYDGNTAVLPALRGYLEAESLDKKKTAMNF-SGW 639
                                                                                                                                                                                                                                                                                                                  232 RRRTITYFDSQRTLNRRCPKHIAKYLQAEAV--KKDRLDFHQGW 273
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DVIKKDMPYFRLRTAKEI 227
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A;Molecule type: DNA
A;Redidues: 1-662 <MIL>
A;Cossidues: 1-662 <MIL>
A;Cossidues: 1-662 <MIL>
A;Cossi-references: EMBL:U23412; NID:9727446; PID:9727449; PIDN:AAA64293.1; CESP:T10F2...
A;Experimental source: strain Bristol N2
R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M. submitted to the EMBL Data Library, February 1998
A; Reference number: 221884
A; Rocession: T39840
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Mollcule Lype: DMA
A; Rosidues: 1-568 < LYNN
A; Residues: 1-568 < LYNN
A; Cross-references: EMBL: AL021839; PIDN: CAA17063.1; GSPDB:GN00067; SPDB:SPBC19G7.09
A; Experimental source: strain 972h-; cosmid c19G7
A; Genetics:
A; Genetics:
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A;Gene: CESP:T10F2.3
A;Introns: 17/1; 51/1; 96/3; 197/3; 291/3; 342/3; 375/2; 619/2; 645/3; 649/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T10F2.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: T16845
R; Miller, N.
Submitted to the EMBL Data Library, March 1995
A; Description: The sequence of C. elegans cosmid T10F2.
A; Reference number: Z18589
A; Accession: T16845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 KKSPHDSTSRKASFRFVQSDQQPARNIVTSDIQNEKSLLLLIRD-LKEKQTESFQDWNEV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRH 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 VLTMDDLGTLYGQNWLNDQVMNMYGDLV----MDTVPEKVHFFNSFFYDKLRTKGYDGV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRWTK---NVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497
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                                                                                                                                                                                                                                                                                                                                                                                                                                       18.0%; Score 319.5; DB 2; Length: 28.7%; Pred. No. 1.6e-18; ive 51; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.2%; Score 268.5; DB 2; Length (Best Local Similarity 26.4%; Pred. No. 3.3e-14; Matches 75; Conservative 53; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 QTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRM----
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Best Local S
Matches 90
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7;

29; Gaps

Length 233; Indels

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C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T37822
R; Deviln, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1997
A; Reference number: 221737
A; Reference number: 221737
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; References: 1-652 < DEV>
A; Experimental source: strain 972h-; cosmid c17A5
C; Genetics:
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                                        12;
                                                                                                       DYLNOKLKFDRSILEFEKDFKRYNEILNERKKIQEDLKKKKEQLAKK-----KLVP--- 405
                                                                                                                                                                                                                                  YGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTK----NVDIFN 210
                                                                                                                                                                                                                                                         265
                                                                                                                                                                                                                                                                                                                                    266 RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKEL 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 ITNTDLTRINGGEFLNDTIVDFYLRYLYCKLOTONPSLANDT-----HIENTFFYNRLTS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 K-----GYDGVKRWTKNVDIFNKELLLIPIHLEVHW------SLISVDVRRR--- 234
                                                                                                                                                         DEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTL 154
                                                                                                                                                                                              406 -ELNEKDDDQVQKALA--SRENTQLMNRDNIE--------ITVRDFKTL 443
                                                                                                                                                                                                                                                                                                                                                                                                                   -----TITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDF 269
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                                          Gaps
                                                                            DHVAQEL-FQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLST 94
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    Length 621;
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Query Match 12.6%; Score 222.5; DB 2; Best Local Similarity 25.2%; Pred. No. 2e-10; Matches 77; Conservative 56; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.6%; Score 205.5; DB 2 26.0%; Pred. No. 5.5e-09; tive 36; Mismatches 72
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A;Introns: 2/2; 105/1; 387/2; 422/2; 501/2
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Best Local Similarity
Matches 60; Conserva
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hypothetical protein AT4g15880 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C; Accession: H85175
R; Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp Nature 402, 769-777, 1999
A; Tille: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; Reference number: A85001; MUID:20083488; PMID:10617198
A; Reference number: A85001; MUID:20083488; PMID:10617198
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-424 <STO>
A; Cross-references: GB:NC_001268; NID:97268336; PIDN:CAB78630.1; GSPDB:GN00140
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A Molecule type: DNA
A? Residues: 1-1034 <0DB>
A: Cross-references: GB:Z47047; EMBL:Z46861; NID:g603997; PID:g763315; MIPS:YIL031w
R; Melluh, P. B.; Koshland, D. E.
Submitted to the EMBL Data Library, May 1995
A; Reference number: S59668
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SMT4 protein - yeast (Saccharomyces cerevisiae)
Nyllternate names: protein Y19905.17; protein Y1L031w
Nyllternate names: protein Y19905.17; protein Y1L031w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 06-Feb-1998
C;Accession: S49947; S59668
R;Odell, C; Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LIQSYQRMPGNAMVRGFRVAYKRHVL------TMDDLGTLYGQNWLNDQVMNMYGD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 IHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKD--RLDFHQGWKG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 GVTDVKKGENFRVEDTSMMLDSLSLDRDVDNDASSLEAYRKLMQS-----AEKRNSKLEA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGQHSPLREEHVTCVQSILDBFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVMDTVPE-----KVHFFNSFFYDKL-RTKGYD--GVKRWTK----NVDIFNKELLLIP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 GTIWARRGAHLAPPDASILISNVCSIGD-----HVAQELFQGSDLGMAEEAERPGEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 12....
23.8%; Pred. No. 1.4e-08;
+ive 56; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: S59668
A, Molecule type: DNA
A, Residues: 1-49. DNA
A, Residues: 1-49. DNA
A, Cross-references: EMBL:U27832; NID:9886765; PID:9886766
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A; Reference number: S49931
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A;Cross-references: SGD:SO001293; MIPS:YIL031w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 YFKMNVARQNN 286
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A; Map position: 4
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Length 1034;

Score 196; DB 2;

11.1%;

Query Match

RESULT 7 H85175

10;

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R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D. P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Gavanagh, T.; Hempell, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; C.; Chalwatzis, N. of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: E71424
A;Acces
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A;Introns: 21/3; 97/3; 123/1; 141/1; 212/2; 279/2; 298/1; 327/2; 407/2; 518/2; 626/2
A;Note: T16L1.110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LIQSYQRMPGNAMVRGFRVAYKRHVL-----TMDDLGTLYGQNWLNDQVMNMYGD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: |: |: |: |: || 187 VVRKQDIELLKPRRFFINDTIIDFYIKYLKNRISPKERGRFHFFINCFFFRKLANLDKGTPS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 GVTDVKKGENFRVEDTSMMLDSLSLDRDVDNDASSLEAYRKLMQS-----AEKRNSKLEA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 LVMDTVPE-----KVHFFNSFFYDKL-RTKGYD--GVKRWTK----NVDIFNKELLLIP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GTIWARRGAHLAPPDASILISNVCSIGD-----HVAQELFQGSDLGMAEEAERPGEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 LGFEIVLNEKKL------SLLRQSRPKTVEKRVEVPREPF-----IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 LTEDEEA----EVYRAFSGRNRRKVLATHENSNIDITGEVLOCLTPSAWLNDEVINVYLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 10.7%; Score 190; DB 2; Length 39 1. Similarity 24.0%; Pred. No. 5.5e-08; 69; Conservative 50; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | |::|||||||: ||||: ||||: ||||: 247 TCGGREAYQRVQKWTKNVDLFEKDYIFIPINCSFHWSLVII 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.2%; Score 163; DB 2; L. Best Local Similarity 31.7%; Pred. No. 2.1e-05; Matches 32; Conservative 21; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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A; Reference number: Z14649 A. Arabidopsis A; Arabidopsis thaliana chromosome 1 BAC T13D8 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AC004473; NID:93108025; PID:93249071; GSPDB:GN00059; ATSP:T13D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: ATSP:TI3DB.11
A;Map position: 1
A:Introns: 106/1; 154/3; 259/2; 275/3; 304/2; 332/2; 366/3; 399/2; 440/2; 478/3; 514/3
                                                    5,
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hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
A;Variety: columbia #sequence_revision 03-Aug-1998 #text_change 11-Jan-2002
C;Accession: E71424
                                                                                                                                                                                                                                                                                                                                                                                                         ---SLI 227
                                                                                                                                                                                                                                                                                                          561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 INVDEEEAQPSTVAEQAAELP--EGLIKLQL-------AIYK---LIVDK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 --GVKRWTKNVDIFNKELLLIPIHLEVHWSLISV-----DVRRRTITYFDSQRTLNRR- 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 LSTDEVVEKLEDIFQQEFSTPSRKGLV-LQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDD 150
                                                                                                               HVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK-----VHFFNSFFYDKLRTKG-
                                                                                                                                                                                                                                                                                                   DYYSNVKKWVNNTDLFSKKYVVIPINISYHWFSCIITNLDAILDFHQNKDKNDAINSDEI
                                                                                                                                                                                                                                                                                                                                                                     SVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMN----VARQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
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Pred. No. 6.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 10.9%; Score 193; DB 2; Similarity 25.9%; Pred. No. 4.7e-08; 67; Conservative 43; Mismatches 85
                                                                                                                                                                                                                                            --YDGVKRWTKNVDIFNKELLLIPIHLEVHW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-547 <VYS>
                                                 33;
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                   27.28;
                                                    52; Conservative
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                   Similarity
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Best Local Si
Matches 67,
                   Best Local
Matches 5
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us-09-848-852a-3.rpr

RESULT 12 T48800 SWH4 related protein [imported] - Neurospora crassa NyAlternate names: protein 15E6.80 C;Species: Neurospora crassa C;Species: Neurospora crassa C;Species: Neurospora crassa C;Accession: T48800 C;Accession: T48800 C;Accession: T48800 A;Schulted, U; Algn, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Nyakatura, submitted to the Protein Sequence Database, April 2000 A;Recension: T48800 A;Steus: preliminary A;Molecule type: DNA A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1240 <sch> A;Residues: 1-1240 <sch> A;Cross references: EMBL:AlJ353822; GSPDB:GN00112; NCSP:15E6.80 A;Experimental source: cosmid contig 15E6; strain 74 A;Cross references: NCSP:15E6.80 A;Map position: 2 A;Introns: 8/3; 358/2</sch></sch>	A;Cross-references: EMBL:U55855; PIDN:AAA98019.1; GSPDB:GN00020; CESP:Y38A8.3 A;Experimental source: strain Bristol N2; clone Y38A8 C\$Genetics: A;Gene: CESP:Y3A8.3 A;Map position: 2 A;Introns: 30/3; 58/3; 91/3; 182/3; 258/1; 288/2; 296/3; 339/3; 437/1; 505/3; 527/3; Query Match A;Introns: 30/3; 58/3; 91/3; 182/3; 258/1; 288/2; 296/3; 339/3; 437/1; 505/3; 527/3; Query Match Best Local Similarity 22 8%; pred. No. 0.005; Matches 65; Conservative 36; Mismatches 88; Indels 96; Gaps 13; QY 87 GSLIPLSTDEVVEKEDIFOOEFSTPSRKGLVLOLIGSYQRMPONAWNGFRV 139
Query Match Best Local Similarity 18.2%; Pred. No. 0.00016; Matches 86; Conservative 50; Mismatches 136; Indels 200; Gaps 14;  Qy 27 LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTY 86	230DVRRTITYEDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQ 682 GAIVDMSNEEASRAAPKCYIPFEDPLSGLDPSKKNHMCHCIKIYLAGLYENTKAP 272 GWKGYPK
SRNMAF RRRNDD DQVMNM D :: ONLLG-	RESULT 14 T19877 hypothetical protein C41C4.6 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T19877 R; Burton, J. Submitted to the EMBL Data Library, February 1995 A; Reference number: 219190 A; Reference number: 219190 A; Recession: T19877 A; Status: preliminary; translated from GB/EMBL/DDBJ
Db 573 TSKVDLLSYDYIIVPVNEYYHWWVAIICNPGKLDPNHPRRSTNSSTSGTETSDSNSTESK 632  Qy 225SLISV	A; Molecule type: DNA A; Residues: 1-342 < WIL> A; Residues: 1-342 < WIL> A; Residues: 1-342 < WIL> A; Cross-references: EMBL: 248045; PIDN: CAA88104.1; GSPDB: GN00020; CESP: C41C4.6 A; Experimental source: clone C41C4 C; Genetics: A; Genetics: A; Genetics: A; Map position: 2 A; Introns: 50/1; 110/3; 144/3; 327/3 Query Match Best Local Similarity 19:6%; Pred. No. 0.012; Matches 63; Conservative 64; Mismatches 138; Indels 57; Gaps 13; QY 23 DASILISNVCSICDHVAQELEGGSDIGMAREBERPGEKAGQHSDLREEHYTCVOSIL 79 C)
RESULT 13 T26650 hypothetical protein Y38A8.3 - Caenorhabditis elegans C;Species: Genorinabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T26650 R;Hallsworth, K. R;Hallswo	Db 23 DVSMREDDLFRMGSTANSGGYADGTHLDGSIGEDDTSSGSNDQHMDFEEDDFDMESSMT 82  Qy 80 DEFLQTYGSLIPLSTDEVVEKLEDIFQGEFSTPSRKGLVLQLIQSYQRMFGNAMVRGFRV 139  ::

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hypotherical protein KO2F2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32915
R;Maggi, L.; Goela, D.
Submitted to the EMBL Data Library, January 1998
A;Description: The Sequence of C. elegans cosmid KO2F2.
A;Reference number: 221246
A;Accession: T32915
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-311 <MAG>
A;Kotossion: T32915
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Residues: 1-311 <MAG>
A;Cross-references: EMBL:AF043699; PIDN:AAB97567.1; GSPDB:GN00019; CESP:K02F2.4
A;Experimental source: strain Bristol N2; clone K02F2
C;Genetics:
A;Genetics:
A;Map position: 1
A;Introns: 16/3; 72/2; 103/3; 139/2; 203/2; 238/2; 273/3
C;Superfamily: Caenorhabditis elegans hypothetical protein K02F2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
142 KRHVLTMDDLGTLYGQNW-----LNDQVMNNYG-----DLVMDTVPEKVHFFNSF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 IVHNPSGAVRRISDVNILDATNKVKSRRLSRRITGHVNCDENAGECRIIIMDSLVHSKKY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 REVIDKTHDSTFDHIRLWLLMSAAATDVDMFCTRFRKVVCOKLPQOKNSVDCGIFMMAFA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 FYDKLRT-------KGYDGVKRWTKNVDIF-NKELLLIPIHLE--VHWSLI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 SV------DVRRRIITYFDSQRTLNRR-----CPK------ 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 RRHIIP-----PLFHNGWVGRNEDRTLLNDTIIEFYMCDWMRLEVFDEATRASSHVFHSF 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.7%; Score 118.5; DB 2; Length 3 Best Local Similarity 19.8%; Pred. No. 0.034; Matches 51; Conservative 35; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 16, 2002, 20:15:46 Job time: 259 secs
                                                                            285 NNDSDCGAFVLQYCKHLALSQP 306
                                                                                                              1: 1: 1: 263 EYFT---KYNTAWQSLP 276
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us-09-848-852a-3.rsp

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GenCore version 5.1.3
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OM protein - protein search, using sw model

December 16, 2002, 19:28:45; Search time 207 Seconds (without alignments) 66.522 Million cell updates/sec Run on:

US-09-848-852A-3 1772 1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	957	_	Q02724 saccharomyc	O13769 schizosacch	P40537 saccharomyc	рошо	homod	Q09275 caenorhabdi							033102 mycobacteri				brady	homo	Q12901 homo sapien	m ger	Q8rgh4 fusobacteri	_		Q97wh0 sulfolobus			P39531 saccharomyc	Q47013 escherichia	$\overline{}$	Q13823 homo sapien	Q57662 methanococc
SUMMARIES	ÇÎ	LP1	ı	ULP1_YEAST	ULP2_SCHPO	ULP2_YEAST	SUS2_HUMAN	SUS1_HUMAN	YQG6_CAEEL	YZ28_METJA	V90K_AMVLE	VPRT_ASFB7	YR22_CAEEL	HTPG_CAMJE	VPRT_ASFM2	DNLJ_MYCLE	FER1_CAEEL	DYHC_EMENI	HUGA_APIME	RP54_BRAJA	TG37_HUMAN	Z155_HUMAN	GGPP_MOUSE	HTPG_FUSNN	RN5A_MOUSE	PAC_ARTVI	RA50_SULSO	SIR2_YEAST	HTPG_BACSU	YJU4_YEAST	ELAD_ECOLI	MPPB_NEUCR	NGP1_HUMAN	Y209_METJA
	Length DB	568 1	659 1		652 1		984 1		342 1					608 1								538 1							626 1					266 1
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	Score	a)	268.5	222.5	205.5	196	170.5	143	124.5	105	97	92.2	90	88	87.5	87.5	87.5	87.5	86.5	86.5	98	85.5	82	82	82	82	82	84.5	84.5	84.5	84	84	84	83.5
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P56966 b geranylge P34036 dictyosteli	058600 methanococc 09vul9 drosophila	QUZUYY SCHIZOSACCH Q57017 haemophilus	01 01	Q9y8g8 penicillium Q05490 pseudomonas	. 01	095749 h geranylge
GGPP_BOVIN DYHC_DICDI	MT52_METJA FUTA_DROME	RAD3_SCHPO YFJD_HAEIN	YLD8_STRCO RSC4_YEAST	TOP2_PENCH	SWI6_YEAST	GGPP_HUMAN
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294 4725	366	2386 420	459 625	1587 353	803	300
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## ALIGNMENTS

P11_	CC use by non-profit institutions as long as its content is in no way
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SEQUENCE
                                                                                                                                               Query Match
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Matches
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          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                       323 DFLQLKGLEISPPPTRPKFIPELEFPDNARKRALKYLNQSNSVSSSEPIITKFNIP---- 378
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                         59 EKAGQHSPLREEHVTCVQS-----ILDEFLQTYGSLIPLSTDEVVEKLEDIFQQ---- 107
                                                                                                                                                                                                                                               ------EFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRH 144
                                                                                                                                                                                                                                                                                       145 VLTMDDLGTLYGQNWLNDQVMNMYGDLV----MDTVPEKVHFFNSFFYDKLRTKGYDGV 199
                                                                                                                                                                                                                                                                                                                                200 KRWTK--NVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYL 257
                                                                                                                                                                                                                                                                                                                                                                      258 QAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKL 317
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                      59;
                                                                                                                                                                 DB 1; Length 568;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
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AAF9771440302D9F CRC64;
  Usaqe
                                                                                                                                                               18.0%; Score 319.5; DB 1; 28.7%; Pred. No. 2.2e-18; tive 51; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein T10F2.3 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659 AA.
modified and this statement is not removed.
          entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                    InterPro; IPR003653; SUMO_protease. Pfam; PF02902; Peptidase_C48; 1. PROSITE; PS50600; ULP_PROTEASE; 1. Hydrolase; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                        EMBL; AL021839; CAA17063.1; -.
                                                                                                                                            64940 MW;
                                                                                                                                                                                      Conservative
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                                                                                                               463
                                                                                                                                                                                                                                                                                                                                                                                                               318 R----- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                   555 RIKMAASIIDAQIY 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                       480 4
527 5
568 AA;
                                                   Q02724; 1EUV.
                                                                                                                                                                           Similarity
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                                                             MEROPS; C48.UPW:
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Submitted (MA)
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Q09353:
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ACT_SITE
SEQUENCE
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YRW3_CAEEL
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XR MEDLINE-97313271; PubMed-9169975;

REDLINE-97313271; PubMed-9169975;

REDLINE-97313271; PubMed-9169975;

Raraujo R., Aparicio A., Barnell B.G., Badcock K., Benes V.,

Araujo R., Aparicio A., Baruckner M., Carpenter J., Cherry J.M.,

Androne D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,

Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,

Androne M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterhoeft A.,

Androne M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

Androne M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

Androne M., Floeth M., Fortin N., Friesen J.D., Fritz C.,

Androne M., Romp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

Androhen M., Bohl T.M., Durnelle D., Schafer M., Scharfe M.,

Andele F.X., Dohl T.M., Durnelle D., Schafer M., Scharfe M.,

Androhen M., Schramm S., Schroeder M., Scharfe M.,

Androhen M., Zollner A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

Malsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,

Androhen M., Schram S., Schroeder M., Hani J.;

Androhen M., Zollner A., Vo D.H., Hani J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 ILSQINSLGIGSAYRGPQRYQNS----YQLSKQKEDKLLEEARIREGHRS------ 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 LISNVCSIG---DHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 QTRG------DRLEDV-----RKRLELQGIAIRPKVEKKKVDDFMALPDAA
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 659;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRRIITYFDSQRILNRRCPKHIAKYLQAEAV--KKDRLDFHQGW 273
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15-UNN-2002 (Rel. 41, Last annotation update)
Ubiquitin-like-specific protease 1 (EC 3.4.22.-).
ULP1 OR YPL020C OR LPB11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 268.5; DB 1; 26.4%; Pred. No. 3.6e-14; iive 53; Mismatches 79;
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                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                              MEROPS, C48.002; -...
WormPep; T10F2.3; CE26951.
Interpro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
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                                                                                                                                                  EMBL; U23412; AAK21468.1; -.
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hes 75; Conservative
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Q02724;
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Wed Dec 18 08:22:17 2002

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SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB. outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                        Mol. Ceil 5:865-876(2000).

-!- FUNCTION: Protease that catalyzes two essential functions in the SUMO pathway: processing of full-length SWT3 to its mature form and deconjugation of SWT3 from targeted proteins. Has an essential role in the G2/M phase of the cell cycle.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 401-621 IN COMPLEX WITH SMT3 MEDLINE-20337970; Pubmed-10882122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 -ELNEKDDDQVQKALA-|-SRENTQLMNRDNIE-------ITVRDFKTL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 YGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTK----NVDIFN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 KELLLIPIHL-EVHWSLISVDVRRRTITYFDS----QRTLNRRCPKHIAKYLQAEAVKKD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 DYLNQKLKFDRSILEFEKDFKRYNEILNERKKIQEDLKKKKEQLAKK-----KLVP--- 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 DEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 DHVAQEL-FQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLST 94
                                                                                                                                                                                                                                          "Ulp1-SUMO crystal structure and genetic analysis reveal conserved interactions and a regulatory element essential for cell growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li S.J., Hochstrasser M.;
Na new protease required for cell-cycle progression in yeast.";
Nature 398:246-251(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72377 MW; F71132817FAF0B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 12.6%; Score 222.5; DB 1; Similarity 25.2%; Pred. No. 1.8e-10; 77; Conservative 56; Mismatches 120;
                                                              MEDLINE=99191836; PubMed=10094048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U36624; AAB68167.1; -. PDB; 1EUV; 07-JUN-00.
                                                                                                                                                                                                                     Mossessova E., Lima C.D.;
Nature 387:103-105(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; C48.001; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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580
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RAGOUTOS J. Poet N. Hajlandean M.A., Lyne M., Lyne R., Stewart A., Bronney J., Peat N., Hayles J., Basham D., Bowman S., Agodouros J., Peat N., Hayles J., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Agodouros J., Peat N., Hayles J., Basham D., Bowman S., Agolone A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Agoneles L., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Holroyd S., Hornsby T., Howarth S., Hurkle E.J., Hunt S., Jagels K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Holroyd S., Moules S., Mungall K., Murphy L., Nibhett D., Odell C., And Holroyd S., Moules S., Standers D., Seeger K., Sharp S., Retvens K., Stevens K., Taylor R.G., Arivey A., Walsh S.V., Warren T., Whitchead S., Stevens K., Taylor R.G., Arivey A., Kalsh S.V., Grymonprez B., Wodward J., Volckaert G., Aerikey R., Stevens K., Enger F., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ber P., Zimmermann W., Wedler H., Mambutt R., Purnelle B., Acadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Austibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Austibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Acatier R., Acatier B., Moenen S., Armstrong J., Forsburg S.L., Ra Boninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S., Armstrong J., Shances P., The genome sequence of Schizosaccharomyces pombe.";

Ry Hatne 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 LTMDDLGTLYGQNWLNDQVMNMY------GDLVMDTVPEKVHFFNSFFYDKLRT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5A4F5D5DE97BD05E CRC64;
                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001) to the SWISS-PROT data bank.
                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ubiquitin-like-specific protease 2 (EC 3.4.22.-).
ULP2 OR SPAC17A5.07C.
652 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY
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Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
Hydrolase; Thiol protease.
                                                                              16-OCT-2001 (Rel. 40, Created)
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    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; C48.UPW; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                         418 KDKDGKRLGHRGVRKWTQKVDLFHKKYIIVPINETFHWYLAIICNIDRLMPVDTKLEEDD 477
                                                                                                   478 EIVMSSVEQPSASKTRQAELTSNSPAILIFDSLANLHKGALNYLREYLLEEAFERKNVHL 537
363 ITNTDLTRLNEGEFLNDTIVDFYLRYLYCKLQTQNPSLANDT-----HIFNTFFYNRLTS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::| | | ::|:|| | : 442 YIIINQDFKCLFNKDWVNDSILDFFTKFYIESSIEKSIIKREQVHLMSSFFTTKLISNPA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                           194 K-----GYDGVKRWTKNVDIFNKELLLIPIHLEVHW------SLISVDVRRR---
                                                                                ----TITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDF
                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycoties;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIR-428BC, A B4972;
BATCALIR-428BC, A B4972;
BATCALIR-428BC, A B4972;
BATCALIR-428BC, A B4972;
BATCALIR-428BC, BAGGOOK K., BARKIET A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Deviin K., Fraser P.
Gentles S., Hamilyn N., Horsnell T.S., Hunt S., Jagels K., Jones N.
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whittehead S.,
Submitted (DEC-1994) to the EWBL/GenBank/DDBJ databases.
--- FUNCTION: INSERTION MUTATION IN SMT4 CONFERS TEMPERATURE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BENOMYL SENSITIVITY; HIGH COPY SUPPRESSOR OF A TEMPERATURE SENSITIVE MUTATION IN MIF2.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                       270 HQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPK-LRR 319
                                                                                                                                                       538 KSTDIRGFHAKVPQQSNFSDCGIYALHFVE-LFLETPEQVIANTLDKSLRR 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03202; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
Hydrolase; Thiol protease.
SEQUENCE 1034 AA; 116882 MW; 782789B3B1DC37F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ubjquitin-like-specific protease 2 (EC 3.4.22.-).
ULP2 OR SWT4 OR YIL031W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 196; DB 1;
Pred. No. 4.7e-08;
                                                                                                                                                                                                                                      PRT; 1034 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMO_protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z46861; CAA86920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA69556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288c / YPH1;
Meluh P.B., Koshland D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1995)
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InterPro; IPR003653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C48.005;
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                     ULP2_YEAST
P40537;
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ULP2_YEAST
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                                                                                                                                                                                                                             618
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUS2_HUMAN STANDARD; PRT; 984 AA.
09B0F6; 09C0F6; Q9HBT5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SUMO-1-specific protease 2 (EC 3.4.22.-) (Sentrin-specific protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O., "Prediction of the coding sequences of unidentified human genes. XI) The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                 SVDVRRRTITYFDSQRTLNRRCPKH1AKYLQAEAVKKDRLDFHQGWKGYFKMN---VARQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain, MEDINE-21154917; PubMed=11230166; MEDINE-21154917; PubMed=11230166; Miemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterfoeft A., Meyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Riein M., Poustka A.; Towards a catalog of human genes and proteins: sequencing and analysis of $500 novel complete protein coding human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gong L., Yeh E.T.;
"SENP7, a novel human sentrin-specific protease.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003653; SUMO_protease.
Para; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; UIP_PROTEASE; 1.
Hydrolase; Thiol protease; Ubl conjugation pathway.
--YDGVKRWTKNVDIFNKELLLIPIHLEVHW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21082932; PubMed=11214970;
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                                                                                                                                                                                                                                                                                                                                                                                619 PNMSDCGVHVI 629
                                                                                                                                                                                                                                                                                                        285 NNDSDCGAFVL 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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us-09-848-852a-3.rsp

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11;
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                                                                                                                                                                                                                                                                                                                                                                                           816 TVSQQSQAQQSQNDNKTIDNDLRTTSTLSLSAEDSQSTESNMSVPKKMCKRPCILILDSL 875
                                                                                                                                                                                                                                                                                                                                                                                                                                           876 KAASVQNTVQNLREYLEVEWEVK--LKTH---RQFSKTNMVDLCPKVPKQDNSSDCGVYL 930
                                                                                                                                                                                                                                          LTMDDLGTLYGQNWLNDQVMNMYGDLVM----DTVPEKVHFFNSFFYDKLRTK---- 194
                                                                                                                                                                                                                                                                                                                                                                                                                          ------YLQAEAVKKDRLDFHQGWKGYFKMN-----VARQNNDSDCGAFV 294
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
MEDLINE-20261527; PubMed=10799485;
KID KIN K.I., Back S.H., Jeon Y.-J., Nishimori S., Suzuki T., Uchida S., Shimbara N., Saitoh H., Tanaka K., Chung C.H.;
"A new SUMO-1-specific protease, SUSP1, that is highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OGGZRI; OGUJVS; O94891;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SUMO-1:specific protease 1 (EC 3.4.22.-) (Sentrin-specific protease SENP6) (Protease FKSG6).
              BY SIMILARITY.

BY SIMILARITY.

R -> K (IN REF. 2).

Q -> H (IN REF. 2).

Q -> H (IN REF. 2).

TRKENNLTEDNPNLS -> MKKFLYIKSVFHTLR (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang Y.-G.; "Identification of FKSG6, a novel protein with protease activity."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                             ------ISVDVRRR---TITYFDSQRT-LNRRCPKHIAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                             Indels 111;
                                                                                                                                                                               DB 1; Length 984;
                                                                                                                                                                                                                                                                                                    ------GYDGVKRWTKNVDIFNKELLLIPIHLEVHWSL------
                                                                                                    REF. 3).
N -> S (IN REF. 1).
Q -> R (IN REF. 1).
A; 317E8B7B4128EDID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeh E.T., Gong L., Kamitani T.;
"Ubiquitin-like proteins: new wines in new bottles.";
Gene 248:1-14(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQYVESFFKDPIVNF---ELPIHLEKWFPRHVIKTKREDIREL 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQYCKHLALSQPFSFTQQDMP------KLRRQIYKEL 325
                                                                                                                                                                             9.6%; Score 170.5; DB 1;
22.6%; Pred. No. 5.1e-06;
Live 41; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND CHARACTERIZATION.
PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 275:14102-14106(2000)
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MEDLINE=20267842; PubMed=10806345;
                                                                                                                                                   112264 MW;
                                                                                                                                                                            Query Match
Best Local Similarity 22.6%
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                   881
984 AA;
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DOMAIN
ACT_SITE
ACT_SITE
CONFLICT
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                   -!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Highly expressed in reproductive organs, such as testis, ovary, and prostate.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                          Nagase T., Ishikawa K. T., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; F., Kotani H., Nomura N., Ohara O.; F., Kotani H., Nomura Sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%; Score 143; DB 1; Length 1112; 30.8%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 LIMDDLGTLYGQNWLNDQVMNMY-GDLVMDTV----PEKVHFFNSFFYDKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    765 765 BY SIMILARITY.
917 BY SIMILARITY.
1030 1030 BY SIMILARITY.
121 121 T -> M (IN REF. 1 AND 4).
1043 1043 Q -> E (IN REF. 1 AND 4).
1105 1106 Y -> C (IN REF. 1 AND 4).
1112 AA; 126144 MW; B6E53875C3833A46 CRC64;
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Hypothetical 35.7 kDa protein C41C4.6 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 -----RTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thiol protease; Ubl conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
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                               MEDLINE=99087487; PubMed=9872452;
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EMBL; AF307849; AAG29831.1; --
EMBL; AF306508; AAG30253.1; --
EMBL; AB018340; EMBJ; AB018340; AB01895; C48.004; --
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(Rel. 35, Last sequ
(Rel. 41, Last anno
SEQUENCE OF 29-1112 FROM N.A.
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917
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SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Burton J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 605003;
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01-NOV-1997
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Q09275;
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ACT_SITE
ACT_SITE
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Best Local Similarity 20.5
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 kDa protein.
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P03593;
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                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                           80 DEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                      ED-----LVDEDEEEEDEEDNDEWTNQKRTDNQNS-----VAYYAAM---EMLR-IRF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AYKRHVLTMDDLGTLYGQNWLNDQVMNMY-GDLVMDTVPE----KVHFFNSFFYD--KLR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VKRWTKNVDIFNKELLLIPIHLEVHWSLISV----D 230
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

MEDLINE-96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 AQARTV-IFDSQLTADLNNLQNMATLI--ESFMKYSYEKRTGNAMPFPLPCILPQRMPQQ 303
                                                                                                                                                                                                                                                                                                                                                 DASILISNVCSIGDHVAQELFQGS---DLGMAEEAERPGEKAGQHSPLREEHVTCVQSIL 79
                                                                                                                                                                                                                                                                                                                                                                              23 DVSMREDDLFRMGSYNSQGYYADGTHLDGSIGEEDETSSGSNDQHMDFEEDDFDMESSMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 VRRRIITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKM-----NVARQ
                                                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                                                                                          ch 7.0%; Score 124.5; DB 1; Length 342; l Similarity 19.6%; Pred. No. 0.007; 63; Conservative 64; Mismatches 138; Indels 57
nitted (JAN-1995) to the EMBL/GenBank/DDBJ databases. SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                      WormPep; C41C4.0; CEVILLE.
InterPro; IRPOS13; SUNG_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; UIL_PROTEASE; 1.
Hypothetical protein; Hydrolase; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJECL28.
Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanocaldococcaceae; Methanocaldococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNDSDCGAFVLQYCKHLALSQP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 TNNFDCGIFIAEFARRFLLSPP 325
                                                                                                                                                            EMBL; Z48045; CAA88104.1; -.
                                                                                                                                                                        MEROPS; C48.UPW; -..
WormPep; C41C4.6; CE01521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 TKGYDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YZ28_METJA
Q60287;
                                                                                                                                                                                                                                                                               Query Mar.
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Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 HVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alfalfa mosaic virus (strain 425 / isolate Leiden).
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cornelissen B.J.C., Brederode F.T., Veeneman G.H., van Boom J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of alfalfa mosaic virus RNA 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%; Score 105; DB 1; Length 1272; Best Local Similarity 25.9%; Pred. No. 1.4; Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.5%; Score 97; DB 1; Length 790; 20.5%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 1272 AA; 149438 MW; 88E7AE8C48629DEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 KNVDIFNKELLLIPIHLEVHWSLISVDVRRRTIT---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001788; RNA_dep_RNApol2.
Pfam; PF00978; RNA_dep_RNApol2; 1.
SEQUENCE 790 AA; 89855 MW; B435C9EB9AA853C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             654 YPVIEVEFKDEKKLFERCSIHIAKNIIGEFCEYILLMFRQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 ----YFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            790 AA.
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Nucleic Acids Res. 11:3019-3025(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83220723; PubMed=6304618;
                                                                                                              Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L77118; AAC37099.1; -. TIGR; MJECL28; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X01572; CAA25728.1; -. EMBL; K02702; AAA46290.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92263807; PubMed-1316688; Garcia-Beato R., Vinuela E.; "A gene homologous to topoisomerase II in African swine fever virus."; Virology 188:938-947(1992).
                                     --PSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYG 169
                                                                                                 397 TTVID--PDKLCMFPDFISEGEVSYFQDYIVGKNPDPELYSDPLGVRSIDSYKHMIKSV- 453
                                                                                                                                                                                                                                                  -----LKPVEDNSLHLE-------RPMPATITYHDKDIVMS-SSPIFLAAAARLMLI 497
               ---IPLSTDEVVEKLEDIFQQEFST- 111
                                                                                                                                                   DLVMDTVPEKVHFFNSF---------FYDKLRTKGYDGVKRWTKNVD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanez R_1J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela E.; "Analysis of the complete nucleotide sequence of African swine fever
                                                                                                                                                                                                                   208 IFNKELLLIPI-----HLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION, CHARACTERIZATION, AND MUTAGENESIS.
MEDLINE-20576431; PUDMed-11031264;
Andres G., Alejo A., Simon-Mateo C., Salas M.L.;
African swine fever virus protease, a new viral member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMO-1-specific protease family.";
J. Biol. Chem. 276:780-787(2001).
-!- FUNCTION: Protease involved in the processing of the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyproteins.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Polyprotein processing peptidase (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              African swine fever virus (strain BA71V) (ASFV)
                                                                                                                                                                                                                                                                                                                                                                                                           273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase, Thiol protease, Late protein.
ACT_SITE 168 168 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
               VQSILDEFLQTYGSL ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M88699; AAA42734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virology 208:249-278(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U18466; AAA65340.1;
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                      263 KKDRL----DFHQ 271
                                                                                                                                                                                                                                                                                                                      498 LRDKITIPSGKFHQ 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A42549; A42549.
MEROPS; C48.050; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10498;
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VPRT_ASFB7
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                                                                                                                                  5,
                                                                                                                                                                                    168 HWVAIEVDMRGDCWSIEYFNS---AGNSPPGPVIRWM--ERVKQQLLKIHHTVKTLAVTN 222
                                                                                                                                                                 223 HWSLISVDVRRR--TITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMN 280
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Transferase; Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
GPRK SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last annotation update)
Putative G protein-coupled receptor kinase W02B3.2 (EC 2.7.1.-).
                                                                                                                                  19;
                                                                                                                                                                                                                                 281 VARQNNDSDCGAFVLQYCK-----HLALSQPFSFTQQDMPKLRRQIYK 323
                                                                                                                                                                                                                                                    223 IRHQRSQTECGPYSLFYIRARLDNVSYAHFISAR---ITDEDMYKFRTHLFR 271
                                                                                              Length 273;
                                                                                                                                44; Indels
                              H->R: LOSS OF ACTIVITY.
C->S: LOSS OF ACTIVITY.
C5AA778179C57C17 CRC64;
                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                  727 AA.
                                                                                                 Score 92.5; D
Pred. No. 2.1;
                                                                                                                                20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000342; Regl_Gprotein.
InterPro; IPR0003290; Ser_thr_pkinase.
Pfam; PF000169; pkinase; 1.
PRINTS; PR00717; GPCRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00133; PH; 1.
SMART; SM00133; PH; 1.
SMART; SM00133; STK_X; 1.
SMART; SM00133; STK_X; 1.
SMART; SM00133; STK_X; 1.
PROSITE; PS00107; PROTEIN_KINASE_APP; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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 POTENTIAL.
                  PROBABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WormPep; W02B3.2; CE02074.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000239; GPCR_kinase.
                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                 31550 MW;
                                                                                                5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U22833; AAA64322.1; -. HSSP; P25098; 1BAK.
                                                                                                                                  29; Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50132; RGS; 1
187
232
168
232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
                                                                 273 AA;
                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
187
232
168
232
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                                                                                                                                                                                                                                                                                                                                                YR22_CAEEL
ACT_SITE
ACT_SITE
MUTAGEN
MUTAGEN
SEQUENCE
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us-09-848-852a-3.rsp

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                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                        211
                                                                                                                                                                                                                                                          EF-----STPSRKGLVLQLIQSYQRM--PGNAMVRGFRVAYKRHVLTMDDLG 152
                                                                                                                                                                                                                                                                                      62 KLGFLLLKDYAENVSESPCPQIKFYEAIKEYEKMETPDERLTKA-REIYDHHIM-VEMLA 119
                                                                                                                                                                                                                                                                                                                                            ELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNR-----RCPK-HIAKYLQAEAVK 263
                                                                                                                                                                                                                                                                                                                                                                                                           165 FLESDKFTRFCQWKNLELNM-OLTMNDFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----H 300
                                                                                                                                                                                          LGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chaperone protein htpG (Heat shock protein htpG) (High temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                          15 MAMEKSRSOPAARASKRIVLPD---PSVRSIMQKFLEKSGDM------KFDKIFNQ
                                                                                                                                                                                                                                                                                                                        153 TLYGQNWLNDQVMNMYGDLVMDTV-PEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 KKRIKMKOGETLALNEHIMLSLVSTGQDCPFIVCMTYAFQSPDKLC--FILDLMNGGDLH
                                                                                                                                                            80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNIT: Homodimer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                           5.1%; Score 90; DB 1; Length 727; 19.7%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: Molecular chaperone. Has ATPase activity (By
                                                                                                                                            ; Pred. No. 11;
50; Mismatches 122; Indels
                                             ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
AA0530D8A9DA57D7 CRC64;
 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 608 AA.
                  C-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                            318 B
83361 MW;
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455
700
175
205
220
                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 KDRLDFHQGWKGYFK--|-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LALSQPFSFTQQDM 314
191
456
54
197
220
318
727 AA;
                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein G).
HTPG OR CJ0518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campylobacter
                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTPG_CAMJE
Q9PHZ3;
                                                                            ACT_SITE
SEQUENCE
                                                                                                                             Query Match
                                             NP_BIND
BINDING
                                                                                                                                            Local
                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     212
                                                                                                                                                         Matches
SHEELES
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and for commercial
                                                                                                                                                                                                                                                                                                                                                                     14;
                (See http://www.isb-sib.ch/announce/
                                                                 R HSSP, POS259;
R HSSP, POS2829; 1AH8.
R HSSP, POS2829; 1AH8.
R InterPro: IPR001504; Arpbind_ATPase.
R InterPro: IPR001404; Hsp90.
DR Pfam; PF00183; HSP90; 1.
DR PRINTS; PR00775; HBATSHOCK90.
DR SWART; SW00387; HATPase_c; 1.
DR PROSITE; PS00298; HSP90; 1.
DR PROSITE; PS00298; HSP90; 1.
FT DOMAIN 332 A; SUBSTRATE-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                          160 KEEQGTSITLYLKDDEFANAY-----KIESIIEKYSNHIQFPIFMEKEEF-TPAKEGEE 212
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        68 REEHVTCVQSIL--DEFLQTYGSLIPLSTDEVVEKLEDIFQ-----QEFSTPSRKG-- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 ---LVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 ISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVAR--- 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 EGKTELKISQINK---ANALWR-----MQKSSLKAEDYERFYEQNFHDSNKPLLY---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 DIVPEKVHFFNSFF-----YDKLRIKGYDGVKRWIKNVDIFNKELLLIPIHLEVHWSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94292916; PubMed-8021596; Daylis S.A., Vydelingum S., Bristow C., Daylis S.A., Vydelingum S., Bristow C., Hammond J.M., Smith G.L., "Nucleotide sequence of a 55 kbp region from the right end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome of a pathogenic African swine fever virus isolate (Malawi LIL20/1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 ----QNNDSDCGAFVLQYCKHLALSQPF-----SFTQQDMPKLRRQIYK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 ELEKLKNNDKE-----KYLSFFKTFGKVLKEGLYGFGGEKDSLLKLMLYK 399
                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   African swine fever virus (isolate Malawi Lil 20/1) (ASFV).
Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
                                                                                                                                                                                                                                                                                                                                  DB 1; Length 608;
                                                                                                                                                                                                                                                                                                                                                                     Indels
Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i-FUNCTION: Protease involved in the processing of the polyproteins (By similarity).
-i-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i-SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                                                                                                                                                                                                     95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polyprotein processing peptidase (EC 3.4.22.-). ORFIGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 AA
                                                                                                                                                                                                                                                                                                                                                   21.1%; Pred. No. 11; ive 45; Mismatches
                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  5.0%; Score 89;
                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Gen. Virol. 7:1655-1684(1994).
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 21.13
nes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                    Query Match
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VPRT_ASFM2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
                                                for commercial
                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).

-!- 609:1007-1011(2001).

-!- FUNCTION: THIS PROTEIN CATALYZES THE FORMATION OF PHOSPHODIESTER
LINKAGES BETWEEN 5'-PHOSPHORYL AND 3'-HUDROXYL GROUPS IN DOUBLE-
STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FOR
THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND REPAIR OF
DAMAGED DNA, EDY SIMILARITY).

-!- CATALYTIC ACTIVITY: NADH(+) + (deoxytibonucleotide)(N) +
(deoxytibopucleotide)(M) = AMP + nicotinamide nucleotide +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Inderes R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 HWSLISVDVRRR--TITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 HIVALFVDMRGDCWSIEYFNS---AGNSPPGPVIRWM--ERVKQQLLKIHHTVKTLAVTN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1769;
        as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MXY-2000 (Rel. 39, Created)
30-MXY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+]).
LIGA OR LIG OR ML1705 OR MLCB637.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY! BELONGS TO THE NAD-DEPENDENT DNA LIGASE FAMILY. SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 VARQNNDSDCGAFVLQYCK-----HLALSQPFSFTQQDMPKLRRQIYK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 IRHQRSQTECGPYSLEYIRARLDNVSYTHFISTR---ITDENMYKFRTHLFR 271
                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.9%; Score 87.5; DB 1; Length 273; 25.0%; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels
                                                Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                          D6AD6DAC62C25F3B CRC64;
use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See P or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches
                                                                                                                                                                                                                                                           ACT_SITE 187 BY SIMILARITY.

ACT_SITE 187 BY SIMILARITY.

ACT_SITE 232 232 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 31493 MW;
                                                                                                                                                                                              EMBL; X71982; CAA50819.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 25.03
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                         232 2
273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
DNLJ_MYCLE
    g
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569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 -LRDGSEREFVMPTTCPECGTTLAPEKEGDADIRCPNARSCPGGLRERVFHVA-SRSALD 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 GSDLGMA-----EEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 IFNKELLLIPIHLEVHWS-LISVDVR-----RRTITYFDSQRTLNRRCPKHIAKY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 MDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 ----KAKTAPL----WRVLVALSIRHVGPTAARALATEFGSVDAILAASPEQLAAVEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50172; BRCT; 1.
PROSITE; PS01055; DNA_LIGASE_N1; 1.
PROSITE; PS01056; DNA_LIGASE_N2; FALSE_NEG.
Ligase; DN repair; DNA replication; NAD; Complete proteome.
DOMAIN 613 677
BRCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLAL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Conservative 37; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMP (BY SIMILARITY).
CFE712B6AFDAA9D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.9%; Score 87.5; DB 1; 3.1%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: December 16, 2002, 19:58:11
Job time: 210 secs
                                                                                           InterPro; IPR001357; BRCT.
InterPro; IPR001357; BRCT.
InterPro; IPR001450; DNA_ligase_OB.
InterPro; IPR001679; DNA_ligase_OB.
InterPro; IPR0003683; HHH_1.
InterPro; IPR004149; Znf_DNAligase_C4.
Ffam; PF00533; BRCT; 1.
Ffam; PF001633; DNA_ligase_DB; 1.
Ffam; PF03119; DNA_ligase_DB; 1.
Ffam; PF03110; DNA_ligase_OB; 1.
Ffam; PF03120; DNA_ligase_OB; 1.
Fram; PF03120; DNA_ligase_OB; 1.
Fram; PF03120; DNA_ligase_OB; 1.
Fram; PF03120; DNA_ligase; 1.
SMART; SM00292; BRCT; 1.
SMART; SM00278; HHH1; 1.
SMART; SM00278; HHH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75912 MW;
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EMBL; Z99263; CAB16425.1;
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SUMMARIES

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Human; secreted protein; treatment; nutritional activity; cytokine; cell proliferation; cell differentiation; hematopoiesis regulation; tissue growth; activin; inhibin; chemotactic; chemokinetic; hemostatic; thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition; gene therapy;

Homo sapiens

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494 CGAATTCCTTCAAACGTATGGCAGCCTCATACCCCTCAGCACTGATGAGGTAGTAGAGAA
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                                                                                                                                                                                                                                                                                                                       This invention describes novel human secreted proteins which are encoded by polynucleotides obtained from fetal brain, adult skin, adult brain, adult thymus and adult aorta cDNA libraries. The adult heart, adult thymus and adult aorta cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating activity, immune stimulating activity, tassue growth activity, activin/inhibin activity, chemotricic/chemokinetic activity, hemostatic and thrombolytic activity, acceptor/ligand activity, and tumor inhibition activity. The invasion suppressor activity, and tumor inhibition activity. The controlleds are also stated to be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ43777-Z43808 represent the polynucleotides described in the invention which encode the proteins represented in AAY50905-Y50947.
                                                                                                                                                                                                                                                    New polynucleotides encoding secreted human proteins, derived from human fetal brain, adult skin, adult brain, adult heart, adult thymus and adult aorta cDNA libraries.
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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             sLeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGlyLeuValLeuGl 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sentrin-specific protease; sentrin; anti-proliferative agent; anti-viral agent; herpes simplex-1; cytomegalovirus; sentrinisation; PML; tumour suppressor; acute promyelocytic leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de-sentrinase; SENP; SENP1; SENP2; SENP3; chromosome 12q13.1;
                                                                                                                                                                                                                                                                                                                                                    140 aTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLe
                                                                                                                 uAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysVa
                                                                                                                                                                                                sArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuIleProIleHisLe
                                                                                                                                                                                                                                                                                           uGluValHisTrpSerLeuIleSerValAspValArgArgArgThrIleThrTyrPheAs
                                                        nLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArgValAl
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/*tag= a
/product= "SENP3"
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                                                                                                                                                                                                                                                                                                                                                                                                                               assays for receptor activity, with the sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed
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Xue AJ,
                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                 Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ Goodrich R, Drmanac RT;
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                                                                                                                                                 Liu C, A
Wang Z, W
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                                                                                                                            (HYSE-) HYSEQ INC.
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Query Match:
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26-DEC-2000;
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Wang J, W
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                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human de-sentrinase (SENP) 3 polypeptide. The specification describes SENP1 and SENP2 polypeptides. The SENP1 gene is found in chromosome 12q13.1 SENP1 is found in the nucleolus, and SENP3 is found in both locations. SENP3 is found in the nucleolus, and SENP3 is found in both locations. SENP polypeptides are sentron-specific proteases that remove sentrin from some sentrinited peptides, but do not affect proteins modified by ubiquitin or NEDDB. SENP polypeptides are used to identify specific modulators of SENP. These modulators are potential anti-proliferative and anti-viral agents such as herpes simplex.1 or cytomegalovirus. SENP polypeptides are used for studying the role of sentrinisation in the biological function of PML, a tumour suppressor implicated in development of acute promyelocytic leukaemia. Fragments of SENP polypucie size used as hybridisation probes and amplification primers for detecting gene expression or preparing mutated sequences.
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                                                                                                                                                                                                                                                                    New polynucleotide encoding de-sentrinase polypeptides, useful antiproliferative or antiviral agents -
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                                                                                                                                                                                                                                                                                                                                Claim 36; Page 120; 122pp; English
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Human secreted protein-encoding gene 11 cDNA clone HOFOB27, SEQ ID NO:60
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aTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLe 160
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ses not include start codon"
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binding partner identification; ss.
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1393 GTGTGCAGCATCGGGGACCATGTGGCCCAGGAGCTTTTTCAGGGCTCAGATTTGGGCATG 1334

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AAD AAD05492-AAD05564 represent cDNAs corresponding to 22 human secreted protein genes, and AAE01672-AAE01743 represent the proteins they encode. AAE01744-AAE01763 represent human secreted proteins they encode. C AAE01744-AAE01763 represent human secreted proteins and their genes are useful for preventing, the secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the c.g. genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, foetal and developmental abnormalities, haematopoietic disorders, foetal and developmental abnormalities, neurological disorders, diseases of the immune system, allergies, neurological disorders, schizophrenia, asthma, allergies, neurological disorders, schizophrenia, asthma, allergies, neurological disorders, schizophrenia, asthma, c.g. parkinson's disease), cognitive disorders, schizophrenia, asthma, allergies, and infections. The proteins can also be used to aid wound disorders, and infections. The proteins can also be used to aid wound contain of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used contained as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alsorders imminished by an approximant of priminished with the disorders or engine and an anity of an anity of an anity disminished by anity and anity an
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                                            /product~ "Mature human secreted protein"
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Human secreted protein-encoding gene 11 cDNA clone HOFOB27, SEQ ID NO:21.
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foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; gene therapy; ss.

Homo sapiens

"Human secreted protein precursor" /product- "Mature human secreted protein" Location/Qualifiers /\*tag= a /product= ' /\*tag= b 522..710 441..521 /\*tag= /\*tag= sig\_peptide mat\_peptide

WO200134767-A2

17-MAY-2001

01-NOV-2000; 2000WO-US30036

99US-0163576 27-JUL-2000; 2000US-0221366 05-NOV-1999;

(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Olsen HS, Shi Y, Soppet DR, Komatsoulis G, 

WPI; 2001-316492/33 P-PSDB; AAE01682 Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition

Claim 1; Page 417-418; 540pp; English.

AAD05492-AAD05564 represent CDNAs corresponding to 22 human secreted protein genes, and AAE01672-AAE01743 represent the proteins they encode.

CC AAE01744-AAE01163 represent human secreted protein fragments or variants.

CT he secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

CC rameliorating medical conditions, e.g., by protein or gene therapy.

CC pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 22 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatond arthritis), inflammation, allergies, neurological disorders schizophrenia, asthma, skin disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, idney disorders, apatrointestinal disorders, pregnancy related disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell collections and also before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognite ligands or binding present sequence represents a human secreted protein-encoding cDNA of partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). invention

quence 1934 BP; 423 A; 542 C; 551 G; 418 T; 0 other;	nt Scores: 6.94e-188 Length: 1934 0.: 1702.00 Matches: 324 Similarity: 97.90% Conservative: 2 cal Similarity: 97.30% Mismatches: 6 atch: 22 Gaps: 0	48-852A-3 (1-332) x AAD05502 (1-1934)	1 MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAla-HisLeuAl 20	TOTACTCTTCCCAATGGCTTTGGGGGACCCCCGGGCCAGAAGGGGAGCGGGGTCTGG	20 aProProAspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGl 40	CCCCCTGATGCCAGCATCTCATCAGCAATGTGTGCGCAATCGGGGACCATGTGGCCC	40 nGluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLy 60	16 GGAGCTATTTCAGGGCTCAGATCTGGGCACCGCAGAAGAGGGCAGAGCGGCCCGGGGAG	60 sAlaGlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAs 80	76 AGCCGGCCAGCACACCCCCTGCGGGAGGAGCATGTGACCTGCGTGCAGAGCATCTTGGA 73:	80 pGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValValGluLy 100	o leaniicticaanciinieecheccicaicciccicaechceaceacheineinean 77	00 sLeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGlyLeuValLeuGl 120 	LeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArgValA		40 aTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLe 160	6 CTACAAGCGGCACGTGCTGACCATGGATGACCTGGGCACCTTATATGGACAGAACTGGC	60 uAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysVa 180 14	/6 CAACGACCAGGTGAAGATGTACGGAGACCTGGTCATGGACACGGTCCCGGAGAAGGT 103	80 1HisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysG1yTyrAsp61yVaLLy 200 	0 sarqTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuleulleProlleHisLe 220		0 uGluValHisTrpSerLeuIleSerValAspValArgArgThrIleThrTyrPh		0 pSerGlnArgThrLeuAsnArgArgCy	6 CTCGCAGCGCACCCTAAACCGCCGCTGCCTAAGCATATTGCCAAGTATCTACAGGCAG	60 uAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAs 280	6 GGCAGTGAAGAAGACCGGCTGGATTCCACCAGGGCTGGAAAGGTTATTTCAAAAT	80 nValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHi 300	6 rerescenssendantarsacasteacresses rerestratarastacresa	30 sLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgArgGl 320
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Note: The sequence data for this patent did not form part of the printed
1396 CCTGGCCCTGTCTCAGCCATTCAGCTTCAGCCAGGAGACATGCCCAAACTTCGCCGGCA 1455
                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J;
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Yang Y,
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                                                                     Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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Wang Z, Wehrman T, Xu C, Xue AJ,
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P-PSDB; AAM41055.
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                               en R, Ma Y, C
u C, Xue AJ,
Drmanac RT;
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system injuries -
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Wehrman T, Xu
Goodrich R,
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Wang Z,
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                              Conservative:
Mismatches:
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The Inventor Leadure Do 247,0 moves insurant ovariation and also encompasses polypeptides 90% identical and polynucleotides 95% identical compasses polypeptides 90% identical and polynucleotides 95% identical compasses polypeptides 90% identical and polynucleotides 95% identical recombinant vectors and host cells comprising human ovarian antigen crecombinant vectors and host cells comprising human ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian orysts, and dysmenorrhoea), endocrine disorders, infertility, disorders of pregnancy, and toxic conjuctories, infertility, disorders of pregnancy, and toxic conjuctories, infertility, disorders of pregnancy, and toxic conjuctories, infertility, disorders (e.g., congenital and acquired incorders, infertility, immune disorders (e.g., congenital and acquired incorders, cophorities, systemic lupus erythematosus, blood-related disorders (e.g., anaemia), cardiovascular disorders, cophorities and urinary system disorders. Ovarian antigen polypeptides and polymerleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may also the used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may also the used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the
                                                                                                                                                                                                                                                                                                                               Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 2175 novel human ovarian antigens (ABP41054-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                        Human ovarian antigen HOFOB27 cDNA, SEQ ID NO:96
rgGlnIleTyrLysGluLeuCysHisCysLysLeuThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 96; 2922pp; English.
                                                                                                                                           BP.
                                                                                                                                           ABQ54216 standard; cDNA; 1933
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                                                                                                                                                                                                                                          (first entry)
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P-PSDB; ABP41139.
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319
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
          userur in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
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polypeptides may be used as food additives or to prepare antibodies
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                                                                                                                                                                                                                              556 ACCCCCTGATGCCAGCATCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCCCA
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                                                                                          Sequence 1933 BP; 423 A; 541 C; 551 G; 418 T; 0 other;
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Mismatches:
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Matches:
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
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                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease, Hauntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful for treating disorders
                                        nValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHi
                                                                                           sLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgArgGl
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Zhang J;
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Yang Y,
                                                                                                                                                             nIleTyrLysGluLeuCysHisCysLysLeuThrval 332
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Xu C, Xue AJ,
, Drmanac RT;
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Wang Z, Wehrman T, Xu C,
Zhou P, Goodrich R, Drman
                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 629
                                                                                                                                                                                                                           AAI58426 standard; cDNA; 2029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000US-0488725.
; 2000US-0552117.
2000US-0588042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0662191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2000; 2000WO-US34263
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P-PSDB; AAM39270.
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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Zhao QA,
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and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
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                                      The sequence data for this patent did not form part of the
                                                                      other;
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                                                                      Sequence 2029
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The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligounclectide complementary
to the complementary strand of a polynuclectide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 3'-end sequence complementary to a
polynucleotide which comprises a 3'-end sequence complementary to a
polynucleotide which comprises a 3'-end sequence therefore the 5'-end sequence/3'-end sequence is selected from those defined in
the 5y-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
che full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH13638 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                     primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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1414 GGCGGTAAAGAAAGACCGACTGGATTTCCACCAGGGCTGGAAAGGTTACTTCAAAATG--
                               nValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHi
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Otsuki
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                                                                                                                                                                                  Hayashi K, Sa
A, Nagai K,
                                                                                                                                                                  sGluLeuCysHisCysLysLeuThrVal
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T, Wakamatsu A,
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2000JP-0183767.
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Sugiyama T,
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09-JUN-2000;
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AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                        439 G; 428 T; 0 other;
                                                                    1578
186
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17
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Mismatches:
Indels:
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                                        Sequence 1578 BP; 339 A; 372
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50.00%
47.45%
46.28%
                     of the present invention.
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Best Local Similari
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nAsnTrpLeuAsnAsp-----

Indels: Gaps: (1-870)

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                                                                                                                                                                                                                                                                                                                                                                 Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker
           GAACTGGCTCAGTGACCAGGTGAGAAGGGTAGAGAAACAGGCCTGAGAGGGGGTTCAGG 1173
                                                                                                  1293
                                                                                                                                  1354 TTTT-----AAGCAGCTTTTTAAGCTCCTTTCATCTTTTTACACAGAGG 1404
                                                     1174 GAGCAGGGTGTCTGGGGCCCTCTGCATGGGGGAGCCCTGTACCCATGCCGCACCCTCCAT 1233
                                                                           174
                                                                                                                        ---GlnValMetAsnMetTyrGlyAspLeuValMetAs
                                                                                                                                                                 185 rPhePheTyrAspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAs
                                                                                                                                                                                                                                                                                                                                            Human neuroblastoma expressed polynucleotide SEQ ID NO 363
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Matches:
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                                                                                                                                                                                                                                                                            AAI94288 standard; cDNA; 870
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Conservative: Mismatches:

Best Local Similarity:

Percent Similarity:

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Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; impuroscictive; antidepressant; nootropic; antidiapathicsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
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                        568 AAGCCGGCCAGCACAGCCCCTTGCGAGAGGAGCATGTGACTTGCGTACAGAGCATCTTTG
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                                                                               20 aProPro-AspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaG
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287 176 407

216 467 256 587 276 644

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Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss; gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
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                       ----AATAGAAAACCA 176
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                                                                                                                                                                                                                                                                                                                                       ProGluLysValHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyr 196
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                                                                  LeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGly
                                                                                                            177 TTTATCAATAGGGAAATAACAAACTATGGGCCAGACATCAAAAATGT-----AAC
                                                                                                                                                                               GlnAsnTrpLeuAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 ysLeuArgArgGlnIleTyrLysGluLeuCysHisCysLysLeu 330
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    AAS25529/c
ID AAS25529 standard; cDNA; 503
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28-MAR-2000; 2000US-0192745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibatcterial; endocrine; cardiant; central nervous system; virucide, antibatcterial; endocrine; cardiant; central nervous system; virucide, antibatcatic; vulnerary; cardiovascular; antidanemic; antiaggregant; haemostatic; vulnerary; cardiovascular; antidanemic; antidapteric; cytostatic; neuroprotective; antidepressant; noctropic; antidabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidapteric; cytostatic; neuroprotective; antidepressant; noctropic; cardiory them can be used in gene therapy, antisense therapy and vaccine cytoduction. The proteins and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatographology, cardiac anaphylaxis, virel, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, cenemical anaemia, plateled discorders, thrombocytopeenia, wounds, burse, ulcers, cenemical anaemia, plateled discorders, immunical anaemia, wounds, burse, anaemia, cenemical anaemia.
genetic disease; haematopoietic disorder; platelet disorder; asthma; thromborytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 ValValGluLysLeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGly 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerIleLeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis, severe combined immunodéficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depressi
Alzheimer's disease, Parkinson's disease, neurodegenerative and
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1148
54
65
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 494; 1217pp; English.
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2000US-0488725.
2000US-0552317.
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755.50
73.19%
53.62%
42.64%
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                                                                                       neurological disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
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                                                                                                                                   Homo sapiens.
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Pred. No.:
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δ g ŏ

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of ovarian cancer. The compositions used not not considered polynucleotides, or immunogenic portions of the proteins, their associated polynucleotides, or immunogenic portions of the proteins. The ovarian tumour polynucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing other genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS2539
                                                                                                                                                                                   The invention comprises compositions used for the therapy and diagnosis
                                                                 New polynucleotides encoding ovarian tumour proteins, useful for
treating ovarian cancer, and as probes, primers, and markers of cancer
progression -
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                                                                                                                                                                                                                                                                                                                                                                                                   represent human ovarian tumour protein cDNA clones.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                  Example 1; page 375; 378pp; English.
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ID AA184371 standard; cDNA; 358 BP
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661.50
88.03%
88.03%
37.33%
                                              WPI; 2001-488879/53
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               Algate PA,
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesls; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          part of the printed directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGTTATGATGGGGTGAAAAGGTGGACCAGAGACGGGGACATCTTCAATAAGGAGCTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 LeulleProlleHisLeuGluValHisTrpSerLeulleSerValAspValArgArgArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrileThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysProLysHisIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4431; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 358 BP; 93 A; 97 C; 89 G; 78 T; 1 other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                     Human polynucleotide SEQ ID NO 4431.
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618.50
86.76%
85.29%
34.90%
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18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                               26-FEB-2001; 2001WO-US04927
                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
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The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar
                                                                                                                                                                                                                                                                                                                                                                                                          Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker for anti-cancer agents
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                                                         241
                                                                                                                                                           257 -----TACTGCAAGCATCTGGCCCTGTCTACACCATTCAGCTTCACCCAGCAGGACATG 310
122 ACCATCACCTATTTGACTCGCAGCGTACCCTAAACCGCCGCTGCCCTAAGCATATTGCC 181
                                                                                    GlyTyrPheLysMetAsnValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheVal 294
                            LeuGlnTyrCysLysHisLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to that for N-myc and TrkA genes.
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                                                                                                   AA193958/c
ID AA193958 standard; cDNA; 820
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Query Match:

US-09-848-852A-3 (1-332) x AA193958 (1-820)

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                              SerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGlnGluLeuPheGln 44
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                                                            GlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLysAlaGlyGlnHis 64
GlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHisLeuAlaProProAspAla 24
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

HSM805332 2269 bp mRNA linear PRI 12-JUL-2002 HOMPO sapiens mRNA; cDNA DKF2p762A152 (from clone DKF2p762A152). AL834294

AL834294.1 GI:21739883

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

RESULT 1 HSM805332 human.

ALIGNMENTS

Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2269)
1 (bases 1 to 2269)
Direct Supmission
Direct Submission
Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY

REFERENCE AUTHORS TITLE JOURNAL

AF199459 Homo sapi AX081143 Sequence AX081143 Sequence AX081143 Sequence AX08164 Mus muscu AF194031 Mus muscu AF194031 Mus muscu AF129071 Pan trog1 AC127468 Papio Cyn AX069229 Sequence AF175325 Homo sapi AC126071 Pan trog1 AC126237 Canis fam AC12632 Securia AC1290725 Homo sapi AC129071 Pan trog1 AC126237 Canis fam AC126239 Felis cat AC130192 Sus scrof AC130192 Sus scrof AC126921 Bos tauru AX209870 Sequence AC099923 Rattus no AL603707 Mouse DNA AC00923 Homo sapi AC06082 Macaca fa AC19115 Rattus no AL806532 Mus muscu AC099244 Rattus no AC099246 Rattus no AC099246 Rattus no BC008589 Homo sapi BC023129 Mus muscu AXB1135 Sequence AX149770 Homo sapi AJ343855 Homo sapi AJ34384 Homo sapi AR368904 Mus muscu BC031652 Mus muscu AC125091 Mus muscu AC119115 Rattus no M22873 Mus musculu AC103148 Rattus no AL806532 Mus muscu Homo sapi Homo sapi Rattus no Mus muscu BC031652 Mus muscu AF260129 Rattus no score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description BC030705 1 SUMMARIES MUSELF4A1 AC103148 AL806532 AX081143 HSM800198 AF1940314 AC016876 AC129071 AC129071 AC127468 AF15325 AC127468 AF15325 AC126237 AC126237 AC126237 AC126237 AC126237 AC126237 AC126237 AC126237 AC126237 AF149770 HSA343855 HSA343584 BC023129 AX081135 AL603707 AK000923 AL806532 AC099294 AB074445 AC099436 BC0308589 BC030705 AC097861 AC125091 AF260129 AB060892 AC119115 AF368904 10 DB 161428 203281 139405 2793 76754 333300 138792 182718 209237 2903 164504 6732 164504 503 184026 Length 2673 173588 000 138792 209237 257644 251835 153553 Match Query Score 442 427.6 426 344.6 333.4 301.6 277.4 260.4 254.6 253.8 251.4 251.4 230.6 183.4 182.4 160.2 143.8 101.4 98.4 96 530.4 486.4 4877.4 469.6 469.6 1843.0 1692.0 83. Result 42 Š υo 00000 000

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This clone (DKFzp762A152) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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PPMEEDGLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASILISNVCSI
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LGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDI
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DH10B: sites NotI + SalI"
/dev_stage="adult"
 from S. Wiemann, Molecular Genome Analysis, German Cancer
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             Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 2258)
Choi,S.J., Jeon,Y.J., Kim,K.I., Nishimori,S., Suzuki,T., Uchida,S., Shimbara,N., Tanaka,K. and Chung,C.H.

Direct Submission
Submitted (28-OCT-1999) Molecular Biology, Seoul National
University, Shillim-dong san 56-1, Seoul 151-742, Korea
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/product="SUMO-1 specific protease 3"
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Cong.L. and Yeh,E.T.
Direct Submission
Submitted (04-OCT-2000) Institute of Molecular Medicine, University of Texas-Houston, 2121 W. Holcombe Blvd. 928, Houston, TX 77030, USA
                                                                                                                              mRNA linear PRI 21-NOV-2000 protease (SENP3) mRNA, complete.
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Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniati
Mammalia; Eutheria; Primates; Catarrh.
1 (bases 1 to 2224)
Yeh,E.T., Gong,L. and Kamitani,T.
Ubiquitin-like proteins: new wines in
Gene 248 (1-2), 1-14 (2000)
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Pred. No. 0;
0; Mismatches
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/chromosome="17"
/map="17p13"
/gene="SENP3"
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PAT 27-FEB-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2206)
Gong, L. and Yeh, E.T.
Composition and methods relating to senp1 - a sentrin-specific
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Patent: WO 0109292-A 9 08-FEB-2001;
Board of Regents, The University of
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Additionation, Vermann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp586K0919) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.blochem.mpg.de/proj/CDNA/.
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                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1782)
Wiemann,S., Well,B., Wellenreuther,R., Gassenhuber,J., Glassl,S., Ansorge,W., Boocher,M., Bloecker,H., Bauersachs,S., Blum,H., Lauber,J., Duesterhoeft,A., Reyer,A., Koehrer,K., Strack,N., Mewes,H.W., Ottenwaelder,B., Obermaier,B., Tampe,J., Heubner,D., Wambutt,R., Korn,B., Klein,M. and Poustka,A.

Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs
                                    1782 bp mRNA linear Fra 1. ..... DKFZp586K0919 (from clone DKFZp586K0919);
                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="bRF2p586K0919"
/tissue_type="uterus"
/clone=lib="586 (synonym: hutel). Vector pSportl; host Odeu_stage="adult"
/dev_stage="adult"
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Martinsried, GERMANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1782)
Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204. .1319
/gene="DRKZp586K0919"
/note="similarity to S.pombe SPBC19G7.09"
/codon_start="
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Pred. No. 0;
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204. .1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .1782
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                                                           Homo sapiens mRNA; cDNA complete cds.
                                                                                                                AL050283.1 GI:4886466
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98.7%;
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Direct Submission
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Matches 1734; Conservative
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                                                                                                                                                                           ORGANISM
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AUTHORS
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RESULT 5
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12 AAAAGCACCTCGCTGACATTCCACTGGAAGCTTTGGGGGCGCCCACCGGGGCCCGGCGGGGG
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                                                                                               354 CCATCCCCCTGTTGTCGTTTTGACTCCCCCCGGGGGCCACCTCCACCCCGGCTGGGTCTG
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WKGYFRMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                       570 g
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                                                                                                                   /codon_start=1
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52. .1758
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Yeh, E.T., Gong, L. and Kamitani, T. Objquitin-like proteins: new wines in new bottles Gene 248 (1-2), 1-14 (2000)
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MKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
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Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1707)

Nishlda, T., Tanaka, H. and Yasuda, H.

A novel mammalian Smt3: specific isopeptidase 1 (SMT3IP1) localized in the nucleolus at interphase

Eur. J. Biochem. 267 (21), 6423-6427 (2000)

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Horinouchi, Hachioji, Tokyo
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GCCTCCCTGCCCCCGGCCATCTTTGATGCCTCAGCTAGTGAAGAAGAAGAAGAAG 238 AGGAGGAGGAGGATGAAGAAGAAGAAGAAGTGGCAGCTTGGAGGCTGCCCCCAAGAT 120	GGAGTCAGCTGGGAACCTCCCAGCGGCCCGCCTTCCCGCCCACTCATCGAAAAACCT 180 	GCTCACAGGGCCGCCGGCGCGTGAGAGCCTTCCGGATGCTGCTCTACTCAAAAGCA 240 	CCTCGCTGACATTCCACTGGAAGCTTTGGGGGCGCCACCGGGGGGGG	CACACCCAAGAACCATTCACCCCAGCAAGGGGTGCGACGCCACAGGTGCCATCCC 360 	CCTGTTGTGTTTTGACTCCCCCGGGGCCACTCCACCCCGGCTGGGTCTGCTAGGTG 420	CTCTCATGGCTGAGGATGGGGTGAGAGGTCTCCACCAGTGCCCTCTGGGCCCCCCATGG 480 	AGGAAGATGGACTCAGGTGGACTCCAAAGTCTCCTGGACCCTGACTCGGGCCTCCTTT 540 	CATGTACTCTGCCCAACGGTTTTGGGGGACAATCTGGGCCCAGAAGGGGAGGCA-CTTGG 599 	CACCCCTGATGCCAGCATCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCC 659	AGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCAGAAGAGGGAGAGGGCCTGGGGAGA 719 	AAGCCGGCCAGCACACCCCCTGCGAGAGGACATGTGACCTGCGTACAGAGCATCTTGG 779 	ACGAATTCCTTCAAACGTATGGCAGCCTCATACCCCTCAGCACTGATGAGGTAGTAGAGA 839 	agciggaggacatititccagcaggagititccaccccitccaggaagggcciggigige 899 	AGCIGAICCAGICITACCAGGGAIGCCAGGCAAIGCIGAGGGGCTICCGAGIGG 959 	CTTATAAGCGGCACGTGCTGACCATGGATGACTTGGGGACCTTGTATGGACAGAACTGGC 1019 	TCAATGACCAGGTGATGAACATGTATGGAGACCTGGTCATGGACACAGTCCCTGAAAAGG 1079 	TGCATTTCTTCAATAGTTTCTTCTATGATAAACTCCGTACCAAGGGTTATGATGGGGTGA 1139
Db 179 Qy 61 Db 239	Oy 121 Db 287	Qy 181 Db 347	Oy 241 Db 407	Qy 301 Db 467	Qy 361 Db 527	Oy 421 Db 587	Qy 481 Db 647	Qy 541 Db 707	Qy 600 Db 767	Qy 660 Db 827	Qy 720 Db 887	Qy 780 Db 947	Qy 840 Db 1007	Oy 900 Db 1067	Qy 960 Db 1127	y 1020 b 1187	1080
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Sirren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Eroke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdomald, P., Marquis, N., McEwan, P., McGurk, A., Mockeran, K., Mochan, K., Santos, R., Santos, R., Sovery, P., Peterson, K., Pollara, V., Riley, R., Santos, R., Santos, R., Sovery, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wayman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Direct, Submission Submitted (08-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles, Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC016876 177703 bp DNA linear HTG 06-AUG-2002
Homo sapiens clone RP11-186b7, *** SEQUENCING IN PROGRESS ***, 10
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 177703)
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Birren, B., Nusbaum, C., Lander, E., Alli, A., Allen, N., Anderson, S., Barien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gardan, L., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
                                                                                                                                                                                                                1426
                                                                                                                                                                                                                                                                                    AAAGGTGGACCAAAAACGTGGACATCTTCAATAAGGAGCTACTGCTAATCCCCATCCACC 1199
                                     ATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCCAAACTTCGTCGGC 1499
                                                                                                                                                                                 TGGAGGTGCATTGGTCCCTCATCTCTGTTGATGTGAGGCGACGCACCATCACCTATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGCGGTAAAGAAAGACCGACTGGATTTCCACCAGGGCTGGAAAGGTTACTTCAAAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCTTTTGTGTTGCAGTACTGCAAGC
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-186B7
Unpublished
2 (bases 1 to 177703)
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Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Nell,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 2, 2002 this sequence version replaced gi:15421989. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22962 AAACTICGECGGCAGAICTACAAGGAGCTGTGTCACTGCAAACTCACTGTGTGAGCCCTCG 22903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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45967 c 46568 g 41254 t 1052
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Best Local Similarity 96.9%; Pred. No. 2.9e-120;
Matches 562; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
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Eukarryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukarryota; Metazoa; Chordata; Catarrhini; Hominidae; Pan.

1 (bases 1 to 164504)

2 Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,

Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,

Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,

Haghighi, P., Hansen, N., Ho, S.-L., Moduro, V.B.,

Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,

McCloskey, J.C., NcDowell, J., Paguirigan, C., Pearson, R.,

Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,

Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,

Wetherby, K.D., Miggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC129071 164504 bp DNA linear HTG 25-JUL-2002
Pan troglodytes clone RP43-149M23, WORKING DRAFT SEQUENCE, 7
                           12902 TACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAAAA 22843
                                                                                                                                    22662 CCTGGGTGGAGCAGTCATCCTCCCCTTCCCCGTGCAGGAGCAGGAAATCAGTGCTGGG 22603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22722 GGGGGTGGCTACAGAAAAGCCCCTTTCTTCCTCTTTTGCAGGGGAGTGTGGCCCTGTGG 22663
                                                                                                                                                                                                                                                                                                                                                                                                                         1846
1547 TACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAAAC 1606
                                                                                                      TCCAGTTCCTTTCCTCTCTTGCCTCTTCCCACTCACTTCCCTTTGGTTTTTCATATTAA 1666
                                                                                                                                                                                                            ATGITICAATITCTGTATTTTTTTTTTTGAGAGAATACTTGTTGATTTCTGATGTGCA 1726
                                                                                                                                                                                                                                                                                                                   GGGGGTGGCTACAGAAAAGCCCCTTTCTTCTTCTTTGCAGGGGAGTGTGGCCCTGTGG 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGGGTGGAGCAGTCATCCTCCCCCTTCCCCGTGCAGGGAGCAGGAAATCAGTGCTGGG
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Contact: nisc_zoo@nhgri.nih.gov
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HTG; HTGS_PHASEL; HTGS_DRAFT.
Pan troglodytes.
Pan troglodytes
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                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 159951 bases at least Q40
Consensus quality: 161126 bases at least Q20
Consensus quality: 161900 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 163904; sum-of-contigs
Quality coverage: 7.39x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence: It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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99.8%; Pred. No. 2.2e-119;
tive 0; Mismatches 1;
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13973. .19270
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19371. .30584
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Pan.

I (bases 1 to 215795)

Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Boutfard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Haghighi, P., Hansen, N., Ho, S.-L., Maduro, V.B., Maduro, V.B., Margulies, E.H., Masiello, C., Maduro, V.B., McCloskey, J.C., McDowell, J., Pagnirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vodt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC127470 215795 bp DNA linear HTG 17-JUL-2002 Pan troglodytes clone RP43-145D13, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                       24696 CTCTCATGGCTGAGGATGGGGTGAGAGGTCTCCACCAGTGCCCTCTGGGCCCCCCATGG 24637
                                                                                                                                                                                                                                                301 CACACCCCAAGAACCATCTTTCACCCCAGCAAGGGGGTGCGACGCCACAGGTGCCATCCC 360
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Submitted (17-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                           14816 CACACCCCAAGAACCATCTTTCACCCCAGGAAGGGGGTGCGACGCCACAGGTGCCATCCC
24936 GCTCACAGCGCCGCCGCCGCCGAGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAAAGCA
                                                                                                     241 CCTCGCTGACATTCCACTGGAAGCTTTGGGGGCGCCACCGGGGCCGGCGGCGGGGGCTTCG
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Center flot name: 145D13

Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319

Consensus quality: 203929 bases at least Q40

Consensus quality: 208855 bases at least Q20

Insert size: 190000; agarose-fp

Insert size: 214395; sum-of-contigs

Quality coverage: 7.30x in Q20 bases; agarose-fp
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Center code: NISC
Web site: http://www.nisc.nih.gov
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                     NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Quality coverage: 6.47x in Q20 bases; sum-of-contigs
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74621. 89522
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89623. 105337
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Cercopithecinae; Papio.
S. Akhter, N., Antonellis, Ayele, K., Beckstrom-Sternberg, S.M.,
S. Akhter, N., Antonellis, Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Madrian, S.D.,
McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC127468 173588 bp DNA linear HTG 17-JUL-2002 Papio cynocephalus anubis clone RP41-263F8, WORKING DRAFT SEQUENCE, 13 unordered pieces. AC127468 AC127468.1 GI:21886864 HTG; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                           Db 205638 GCCTCCCTGTCCCCCGACCCTCTTTTGATGCCTCAGCAAGTGAAGAGAGAAGAAGAAGAGGG 205697
                                                                                                                                                                                                                                                                                                                                                       Db 205698 AGGAGGAGGAGGATGAAGATGAAGAGGAGGAAGGAGCTAGCAGCTTGGAGGCTGCCCCCAAGAT 205757
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                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                           AGGAGGAGGAGGATGAAGATGAAGAGGAGGAAGTGGCAGCTTGGAGGCTGCCCCCAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 205758 GGAGTCAGCTGGGAACCTCCCAGCGCCCCCCTTCCCGCCCACTCATCGAAAAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 206058 CTCTCATGGCTGAGGATGAGGGTGAGGGTCTCCACCACTGCCCTTGGGCCCCCCATGG
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Papio cynocephalus anubis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 206118 AGGAAGATGGACTCAGGACTCCAAAGTCTCCTCTGGACCCTGACTCGGG 206169
                                                                                                                            Length 215795;
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                                                  1511 others
                                                                                                                                                                           Indels
                                                                                                                       Score 530.4; DB 2;
Pred. No. 2.3e-119;
0; Mismatches 1;
                       /note="assembly_fragment"
52160 a 54859 c 53752 g 53513 t
166903. .215795
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                                                                                                                            26.6%;
99.8%;
                                                                                                                         Query Match 26.6%
Best Local Similarity 99.8%
Matches 531; Conservative
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                                               BASE COUNT
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AUTHORS
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                                                             Sequencing Center, 8717
                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid: n/a: 100% of reads
Sequencing vector: plasmid: n/a: 100% of reads
Sequencing vector: plasmid: n/a: 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 16/0890 bases at least Q40
Consensus quality: 16/086 bases at least Q30
Consensus quality: 16/000; agarose-fp
Insert size: 177000; agarose-fp
Insert size: 17388; sum-of-contigs
Quality coverage: 6.54x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....gth .....gth ....
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139303: gap of unknown length
14 173588: contig of 34285 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 11566 bp in length
gap of unknown length
contig of 9729 bp in length
gap of unknown length
contig of 17601 bp in length
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84235: contig of 15715 bp in length
84335: gap of unknown length
122003: contig of 27668 bp in length
12103: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2699: contig of 2699 bp in length 2799: gap of unknown length 7344: contig of 4545 bp in length 7444: gap of unknown length 11555: contig of 4111 bp in length 11655: gap of unknown length
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/organism="Papio cynocephalus anubis"
/db_xref="taxon:9555"
                                                                                                                                              Center: NIH Intramural Sequencing Center
Center code: NISC
                        Direct Submission
Submitted (17-JUL-2002) NIH Intramural Seq
Grovemont Circle, Gaithersburg, MD 20877,
                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                        Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
Center project name: cyr
Center clone name: 263F08
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/note="assembly_fragment"
|11656. 1527
/note="assembly_fragment"
|15328. 19720
/note="assembly_fragment"
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/clone_lib="RP41"
1. .2699
/note="assembly_fragment"
2800. .7344
/note="assembly_fragment"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                       26.2%; Score 522.4; DB 2; 98.9%; Pred. No. 2.1e-117; iive 0; Mismatches 6;
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WO0102594.
                                             29325. .40890
/note="assembly_fragment"
40991. .50719
/note="assembly_fragment"
/note="assembly_fragment
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AX069229
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                clone_end:SP6
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Matches 526; Conservative
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multiple regulatory elements that direct high-level reporter gene expression in mammalian cell lines Genomics 62 (3), 468-476 (1999)
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4773. .5193
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5249. .>6732
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="eukaryotic initiation 5249. .5286
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/gene="EIF4A1"
/note="ribosome component"
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                                                                                                                                             1. .6732
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="EIF4Al"
/product-
                                                                                                                                                                                                                         /rpt_family="Alu I"
/rpt_type=dispersed
151. .1823
/rpt_family="Alu I"
/rpt_family="Alu I"
                                                                  2 (bases 1 to 6732)
Greaves,D.R. and Catchpole,I.
Direct Submission
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                                                                                                                                                                                                              /clone="cosCD68C1"
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                                                                                                                                                                                                                                                                                                                                             /rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="EIF4A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                /map="17p13"
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ilarity 94.9%;
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                                                                                                                                                                                                                                                               CAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCTGAGGAGGACATGCCC 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGGGTGCCTACAGAAAAGCCCCTTTCTTCCTCTGTTTGCAGGGGAGTGTGGCCCTGTG 1785
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HOMO Sapiens eukaryotic initiation factor 4AI (EIF4A1) gene,
partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                    4187 GCCTGGGTGGAGCAGTCATCCTCCCCCTTCCCCGTGCAGGAGCAGGAAWTCAGNGATG
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                                                                                                                                                                                    11;
                                                                                                                                                           Length 5318;
                 and Ford, M.J.
                                                                                                                      others
                                                                                                                                                                                    Indels
 1 (bases 1 to 5318)
Greaves, D.R., Thomsen, L., Catchpole, I.R. and For Dna constructs based on the eif4a gene promoter Patent: WO 0102594-A 40 Il-JAN-2001;
GLAXO GROUP LIMITED (GB).
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                                                                                                                                                          Score 486.4; DB 6;
Pred. No. 9.8e-109;
1; Mismatches 17;
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                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
1210 c 1423 g 1350
                                                                  Location/Qualifiers
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AF175325.1 GI:696997
                                                                                                                                                          Query Match 24.4%;
Best Local Similarity 94.9%;
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        Pathology,
Submitted (03-AUG-1999) Sir William Dunn School of Patholog
University of Oxford, South Parks Road, Oxford OX1 3RE, UK
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             3868. 4120
/note="similar to murine eIF-4AI gene"
4259. 4334
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 164504)

Rakhter, N., Antonellis, A., Ayele K., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,

Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,

Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,

Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,

Marguiles, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,

Mcloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,

Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,

Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

I. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC129071 164504 bp DNA linear HTG 25-JUL-2002 Pan troglodytes clone RP43-149M23, WORKING DRAFT SEQUENCE, 7 unordered pieces.
4095 AGGGGATGGCTACAGAAAGCCCCTTTCTTCCTCTTTGCAGGGGAGTGTGGCCCTGTG 4154
                                                                                                                                               1786 G-CCTGGGTGGAGCAGTCATCCTCCCCCTTCCCCGTGCAGGGAGCAGGAAATCAGTGCT- 1843
                                                                                                                                                                       GGGGGTGGTGGGCGGACAATAGGATCACTGCCTGCCAGATCTTCAAACTTTTATATAT 1903
                                                                                                                                                                                                                                                         Direct Submission
Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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Center clone name: 149M23

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 159991 bases at least Q40
Consensus quality: 161126 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 163904; sum-of-contigs
Quality coverage: 7.39x in Q20 bases; sum-of-contigs
Quality coverage: 8.34x in Q20 bases; sum-of-contigs
                                                             AGGGGGTGGCTACAGAAAAGCCCCTTTCCTCTCTGTTTGCAGGGGAGTGTGGCCCTGTG
                                                                                 Center: NIH Intramural Sequencing Center
Center code: NISC
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Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135883 TCCAGTTCCTTCCTCTCTTGCCTCTTCCACTCACTTCGTTTTCATATTAA 135942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135943 ATGTTTCAATTTCTGTATTTTTTTTTTTTTTGAGAAATACTTGTTGATTTCTGATGTGCA 136002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD 135763 AAACTTCGTCGGCAGATCTACAAGGAGCTGTGTCACTGCAAACTCACTGTGTGAGCCTCG 135822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135823 TACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAAAC 135882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1487 AAACTTCGTCGGCAGATCTACAAGGAGCTGTGTCACTGCAAACTCACTGTGTGAGCCTCG 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAAAC 1606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                      contig of 3137 bp in length contig of unknown length contig of 10635 bp in length of app of unknown length contig of 5298 bp in length contig of 11214 bp in length gap of unknown length gap of unknown length contig of 14618 bp in length contig of 31268 bp in length contig of 31268 bp in length
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Pred. No. 2.4e-106;
0; Mismatches 6;
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42831 c 41755 g 40472 t

    164504
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Best Local Similarity 98.6%;
Matches 492; Conservative (
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, O.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D., NISC. Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                         AC126925 161428 bp DNA linear HTG 10-JUL-2002 Canis familiaris clone RP81-332E11, WORKING DRAFT SEQUENCE, 15
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Db 136003 GGGGGTGGCTACAGAAAAGCCCCTTTCTTCCTCTGTTTGCAGGGGAGTGTGGCCCTGTGG 136062
                                                                                                                                              Db 136123 GGTGGTGGGCGGACAATAGGATCACCCTGCCAGATCTTCAAACTTTT-TTTTTA 136181
                                                                                                                      Center clone name: 332E1
Center clone name: 332E1
Center clone name: 332E1
Sequencing vector: plasmid; n/a; 100% of reads
Cenmistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 148712 bases at least Q40
Consensus quality: 151471 bases at least Q30
Consensus quality: 153125 bases at least Q20
Insert size: 152000; agarose-fp
Insert size: 160028; sum-of-contiss
Quality coverage: 5.36x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: cwp
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                     unordered pieces
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AC126925/c
LOCUS
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JOURNAL
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KEYWORDS
SOURCE
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Gaps
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unknown length
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contig of 8629 bp in length
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of 8902 bp in length
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Pred. No. 1.3e-105;
0; Mismatches 36;
                                                                                       unknown leng
of 3852 bp i
unknown leng
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7426 .12261
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102276. .131685
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93.2%;
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Best Local Similarity 93.2
Matches 496; Conservative
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88256
88136
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                                121 GGAGTCAGCTGGGAACCTCCCAGCGGCCCCGCCCTTCCCGCCCCACTCATCGAAAAACCT
                                                GCTCACAGCGCCGCCGCCGAGCCATGAGGCCTTCCGGATGCTGCTCTACTCAAAAAGCA
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Search completed: December 16, 2002, 17:29:13 Job time : 6622 secs us-09-848-852a-3.rst

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16154066 seqs, 8097743376 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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em\_estpl:\*
em\_estro:\*
em\_htc:\*
gb\_estl:\* em\_esthum:\* gb\_est2:\*
gb\_htc:\*
gb\_est3:\*
gb\_est4:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ion	1 0 0 0 0 F H		AL57820 AL57820 BI152305 60291742 BM607574 ih41e03.y AW643059 cm25f04.w BF139554 601785671 AQ978128 RPCI-23-3 BF954315 QV2-NN004 BI392544 pgpln.pk0 AW825381 usl4e04.y		BL147525 602960160 BC000958 Homo sapi AF335474 Homo sapi A1148063 gg61g06.r A1261629 g230e09.x BM941363 01-M-B21- BI017569 PM3-ET027 BM555097 AGENCOURT BG083248 H3086B07-	v ~ 4 ~ 0 ° 4	mRNA linear EST 05-MAR-2002 mo sapiens cDNA clone IMAGE:5548958 raniata; Vertebrata; Euteleostomi; atarrhini; Hominidae; Homo
WW.	4 BM80655 2 BG87052 2 BG87052 2 BG86570 3 BI45621 4 BM69666	4470000	9 AL5/8220 13 BL152305 10 AW642059 12 BF139554 17 AQ9/8128 13 BF954315 10 AW825381	04m 044	3 BI2475 1 BC0009 1 AF3354 1 AI14806 AI14806 AI16162 4 BM9413 3 BH0175 3 BM5550	14 B0261255 13 BM185366 14 BQ39444 14 BQ395166 10 AW961869 12 BF443604 ALIGNMENTS	1071 bp MGC_72 Ho 2 ordata; C imates; C .nih.gov/
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/tab.host="DH10B (phage-resistant)"
/hote="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Sydrange insert size 2 kb. Library constructed by Life
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                                               cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM12258 row: 1 column: 15
Plate: LLAM12258 row: 1 column: 15
High quality sequence stop: 648.
1. 1071
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        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5548958"
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AGENCOURT_6542932 NIH_MGC_72 Homo sapiens CDNA clone IMAGE:5548865
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MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHis-LeuAl
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="Inbags: 4922696"
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/lab_host="DH10B (TI phage-resistant)"
/note="Corpan: sallyary pland; Vector: pCMV-SPORT6; Site_1:
NotI: Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

a 195 c 202 g 184 t
                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLAM10842 row: n column: 09
High quality sequence stop: 789.
Location/Qualifiers
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  Health, Mammalian Gene Collection (MGC)
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musculus cDNA clone IMAGE:4922696 5',
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NIH-MGC http://mgc.nci.nih.gov/.
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                               aProProAspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGl
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AUTHORS TITLE JOURNAL

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"SM Mus musculus.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Murinae; Mus.

E 1 (bases 1 to 985)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1637 row: o column: 24

High quality sequence stop: 746.

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Location/Qualifiers

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                                                                                                                                                                                                                                                                               149 AspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnAspGlnValMetAsnMetTyr 168
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                                                                                     ProGlyAsnAlaMetValArgGlyPheArgValAlaTyrLysArgHisValLeuThrMet
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIGO99 row: j column: 19
High quality sequences stop: 728.
Location/Qualifiers
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BG865703
BG865703.1 GI:14216243
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Mus musculus
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Best Local Similarity:
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Query Match:

29

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Pred. No.:

COUNT

BASE CO ORIGIN

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451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9565
Email: msoares@Ublue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                         1 (bases 1 to 626)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                              Contact: Soares, MB Program for Rat Gene Discovery and Mapping
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/db_xref="taxon:10090"
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/clone="InAGE:5252591"
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/ib_rary constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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BQ898865
BQ898865.1 GI:22290891
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Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
MIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM13564 row: o column: 14
High quality sequence stop: 614.
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                                                                     192 ArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsnValAspIlePheAsnLys
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'Organism="Homo sapiens"

/db.xref="texon:9606"

/clone="IMAGE:6181093"

/clone_lib="Lupski_dorsal_root_ganglion"
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/note="Vector: pcMv-spoRr6 (Life Technologies); Site_1:
NotI: Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGGTCGC-3' and
5'-TCGACCACGCGTCGC-3' and
5'-TCGACCACGCGTCGC-3' and
1' Kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies.
a 238 c 220 g 235 t
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Homo sapiens cDNA clone IMAGE:5554637
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AGENCOURT 6492923 NIH_MGC_85
5', mRNA sequence.
BM804530 GI:19121353
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                          /clone_lib="NIH_MCC_85"
/tissue_type="lymphoma, cell line"
/tasue_type="lymphoma, cell line"
/lab_host="lymphoma, cell line"
/lab_host="lymphoma, cell line"
/note="Gran: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Into this is a NIH_MGC Library."
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                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAML2273 row: i column: 06
High quality sequence stop: 583.
Location/Qualifiers
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Mismatches:
Indels:
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                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5554637"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Sciurognathi; Muridae; Murinae; Mus. 2. 1 (bases 1 to 667)

S. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

M. Mouse whole genome caffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 30, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 03-OCT-2000
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1M0164L10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0164L10 R, DNA sequence.
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
180
                                                                                                                                                                   795
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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/clone="UUGC1M0164L10"
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of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/tissue_type="mix - brain, ovary, placenta, kidney, lung,
liver, embryo, heart, muscle, spleen"
/lab_host="SOLR"
                             Euteleostomi;
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Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contact the ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pBlueScript SK(-); Site_1:
Xhol; Estimated insert size approx.1 kb"
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187
4
7
1
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Contact: Lee, NH
The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 208 Tel: (301) 838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contel#703-365-2700 for further information Seq primer: M13 Reverse.
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:10116"
/clone="RGIDW31"
/clone_11b="Rat gene index, n
Bento Soares"
                                                                       1 (bases 1 to 616)
Lee.N.H., Glodek,A., Chandra,I., M
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpsorelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0249-120100-022-c03&t3=2000-01-12&t4=1)
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 620)
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
For Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/db_xref="taxon:9606"
/clone_lib="CT0249"
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-CT0249-
290100-022-c03&t3=2000-01-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 583.
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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8
GAATTCCTTCAAACGTATGGCAGCCTCATACCCCTCAGGACTGATGAGGTAGTAGAGAAG
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/clone_lib="CT0249"
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Tel: +55-11-2704922
Fax: +55-11-2707001
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/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /106 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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High quality sequence stop: 499.

High quality sequence stop: 499.

Location/Qualifiers

1. :572

/organism="Homo sapiens"
/db_xref="taxon:9606"
//clone_lib="Br0604"
//clone_lib="Br0604"
//oret="Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A min!-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

NT 140 a 143 c 149 g 140 t
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-BT0604-150 200-031-E07&t3=2000-02-15&t4=1)
Seq Primer: puc 18 forward
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 573)
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2 (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
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20202663
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/db_xref="taxon:9606"
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/clone=lib="LII_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCWNSPORT 6; Site_1: NotI; 1st strand cDNA
was prined with NotI-ollgo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCWNSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp mRNA linear EST 16-FEB-2001 sapiens cDNA clone CS0DK002YD13 3
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275
                                                                                                                                                            379
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                   256 TyrLeuGlnAlaGluAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGly
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Bummania; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 626)
1 (bases 2 to 626)
1 (bases 3 to 626)
1 (bases 3 to 626)
1 (bases 4 to 6
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AL578220
AL578220.1 GI:12942089
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870 bp mRNA linear EST 05-JUL-2001
602917742F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5067995 5',
mRNA sequence.
B1152305
B1152305.1 G1:14612306
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:5067995"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Paraged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMIII83 row: d column: 12
High quality sequence stop: 523.
Location/Qualifiers
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                                            GlyGlnasnTrpLeuAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThr
                                                                                         565 GGACAGAACTGGCTCAATGASCAGGTGATGAACATGTATGGAGACCTGGTCATGGACACA
                                                                                                                                                                                                                                                                                                                                      IleProIleHisLeuGluValHisTrpSerLeuIleSerValAspValArgArgThr
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene (Mubblished (1999)
Contact: Robert Strausberg, Ph.D.
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/organism="Mus musculus"
/strain="CZECH II"
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house mouse.
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Stem cell origin."

/hab_nost_nHil08
//note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
1 247 c 190 g 201 t
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Best Local Similarity:
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
         AAD05540
AAF55961
AAI94288
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AAI61446
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                                                              December 16, 2002, 14:18:34; Search time 397 Seconds
         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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DNA transcription
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Tomato pest resist Promoter of gene r Mlal2 nucleotide s

Tumour suppressor

2000US-0488725. 2000US-0552317. 2000US-0598042. 2000US-065312. 2000US-0653450. 2000US-0653191. 2000US-0653191.

21-JAN-2000; 25-APR-2000; 209-JUL-2000; 219-JUL-2000; 203-AUG-2000; 214-SEP-2000; 219-OCT-2000; 2

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                                                                                                                                                                                                                                                                Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                           and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Yang Y,
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Xue AJ,
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                                                                                                                        such as central nervous system injuries
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                                       Chen R,
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                                      Asundi V, Che
Wehrman T, Xu
Goodrich R,
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98.9%;
29-NOV-2000; 2000US-0727344
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Matches 1967; Conservative
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P-PSDB; AAM39269.
                                      Liu C, A
Wang Z, W
Zhou P,
                   (HYSE-) HYSEQ INC
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Wang J, W
Zhao QA,
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Wed Dec

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The present sequence encodes a human de-sentrinase (SENP) 3 polypeptide.
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                                                                                                                                                                       SENP; SENP1; SENP2; SENP3; chromosome 12q13.1;
                                                                                                                                                                                                                                                                                                                             sentrin-specific protease; sentrin; anti-proliferative agent;
anti-viral agent; herpes simplex-1; cytomegalovirus; sentrinisation;
PML; tumour suppressor; acute promyelocytic leukaemia; ss.
        GTCATCCTCCCCCTTCCCCGTGCAGGAGCAGGAAATCAGTGCTGGGGGGTGGTGGCGGGA
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The specification describes SENP1 and SENP2 polypeptides. The SENP1 gene is found in chromosome 12q13.1. SENP1 is found in the nucleolus, and SENP3 is found in the nucleolus, and SENP3 is found in the nucleolus, and SENP3 is found in both locations. SENP polypeptides are sentron-specific proteases that remove sentrin from some sentrinised peptides, but do not affect proteins modified by ubiquitin or NEDDBS. SENP polypeptides are used to identify specific modulators of SENP. These modulators are potential anti-proliferative and anti-viral agents such as herpes simplex-1 or cytomegalovirus. SENP polypeptides are used for studying the role of sentrinisation in development of acute promyelocytic leukaemia. Fragments of SENP polypedides are used as hybridisation probes and amplification prologoral function of PML, a tumour suppressor implicated in development of acute promyelocytic leukaemia. Fragments of SENP polypucided as nybridisation probes and amplification primers for detecting gene expression or preparing mutated sequences, also as antisense sequences for inhibiting SENP expression.
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Pred. No. 0;
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invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic, acids may expect acitivity. The polymucleotides are useful some therapy. A composition containing a polypeptide or polymucleotide in invention may be used to treat diseases of the peripheral nervous injuries, peripheral nervous sized neuropathies and central nervous system diseases, such as alised neuropathies and central nervous system diseases, such as leadiner's, Parkinson's disease, Huntington's disease, amyotrophic real sclerosis, and Shy-brager Syndrome. Other uses include the lisation of the activity, chemotactic/chemokinetic activity, haemostatic thromholytic activity, cancer diagnosis and therapy, drug screening, thromholytic activity, arthritis and inflammation, leukaemias and
nootropic; immunosuppressant; cytostatic; gene therapy; cancer; ral nervous system; neuropathy; central nervous system; CNS; er's; Parkinson's disease; Huntington's disease; haemostatic; phic lateral sclerosis; Shy-Drager Syndrome; chemotactic; netic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel human secreted proteins which are encoded by polynucleotides obtained from fetal brain, adult skin, adult brain, adult thymus and adult acrta cDNA libraries. The colling and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hematopolesis regulating cettivity, tassue growth activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumor invasion suppressor activity, and tumor inhibition activity. The polynucleotides are also stated to be useful for gene therapy.

AA243777-243808 represent the polynucleotides described in the invention which encode the proteins represented in AAV50905-V50947.
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                                                                                                                               Human; secreted protein; treatment; nutritional activity; cytokine; cell proliferation; centapopolesis regulation; tissue growth; activin; inhibhi; chemotactic; chemokinetic; hemostatic; thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding secreted human proteins, derived from human fetal brain, adult skin, adult brain, adult heart, adult thymus and adult aorta cDNA libraries.
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                                              TGTTTCAATTTCTGTATTTTTTTTTTTTGAGAGAATACTTGTTGATTTCTGATGTGCAG
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29-NOV-2000;
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  Wang D;
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Ren F,
Zhang J
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Yang Y,
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Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                    nucleic acids and polypeptides, useful is central nervous system injuries -
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0; Mismatches
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Asundi V, Che
Wehrman T, Xu
Goodrich R,
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Best Local Similarity 97.1%;
Matches 1719; Conservative
                                                                                                     WPI; 2001-442253/47.
P-PSDB; AAM41055.
Liu C, P
Wang Z, F
Zhou P,
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           CATCTTGGACGAATTCCTTCAAAC-GTATGGCAGCCTCATACCCCTCAGCACTGATGAGG
                                                 TCCGAGTGGCTTATAAGCGGCACGTGCTGACCATGGATGACTTGGGGACCTTGTATGGAC
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Yang Y,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                                                                1958 AAATGCCACGGTCCTGCTCTGGTCAATAAAG 1988
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2000US-055317.
2000US-0598042.
2000US-065312.
2000US-0653450.
2000US-0653450.
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19-JUL-2000;
03-AUG-2000;
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25-APR-2000;
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Wang J, V
Zhao QA,
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Best Local Similarity 97.1%;
Matches 1719; Conservative
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C.N.S disorders.
Note: The sequence data
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Conservative

Matches 1672;

food additive;

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356 310 416 370 476 430 536

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AARD05492-AAD05564 represent cDNAs corresponding to 22 human secreted protein genes, and AAE01672-AAE01743 represent the proteins they encode. CC AAE0174 AAE01163 represent human secreted protein fragments or variants. CT he secreted proteins and their genes are useful for preventing, treating corrected proteins and their genes useful for preventing, treating corrected proteins can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 22 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune CC diseases (e.g., rheumanatoid arthritis), inflammation, allergies, neurological disorders schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, and giogenic disorders, indiapered disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell
                   angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
The present sequence represents a human secreted protein-encoding cDNA of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to requencate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                 "Human secreted protein precursor"
neurological disorder; Alzheimer's disease;
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27-JUL-2000; 2000US-0221366.
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Score 1451.2; Pred. No. 0;

72.9%; 89.2%;

Best Local Similarity

Query Match

1015

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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; tumour; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
inflammatory condition; immune disorder; blood disorder;
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                                                                                                    Human ovarian antigen HOFOB27 cDNA, SEQ ID NO:96.
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polyucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen.

The combinant vectors and host cells comprising human ovarian antigen of ovarian antigens and polyucleotides and polypeptides in diagnosing.

The ating, prognosing or preventing various ovary and/or breast-related alsorders such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, coplycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), chlood-related disorders (e.g., anaemia), cardiovascular disorders, and uniany system disorders, neurological disorders, gastrointestinal disorders and uniany system disorders, ovarian antigen polypeptides and polyputcleotides may also be used in screening for compounds which modulate varian antigen perpension or activity, The polynucleotides may
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the obypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, dury targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  printed
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neurological disorder;
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                      gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; sanithody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 24; Length 1933;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177;
    cardiovascular disorder; respiratory disorder;
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89.2%;
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P-PSDB; ABP41139.
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              TTGCAGCTGATCCAGTCTTACCAGCGGATGCCAGGCAATGCCATGGTGAGGGGCTTCCGA
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NO: 60 Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatiod arthritis; inflammation; allergy; neurological disorder; AIDaeimer; s disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; endocrine disorder; pregnancy related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; ss. 1667 Human secreted protein-encoding gene 11 cDNA clone HOFOB27, SEQ ID 1210 TTCGACTCGCAGCGCACCTAAACCGCCGCTGCCCTAAGCATATTGCCAAGTATCTACAG TTTGACTCGCAGCGTACCCTAAACCGCCGCTGCCCTAAGCATATTGCCAAGTATCTACAG CCAGTTCCTTTCCTCTTGCCTCTTCCCACTCCACTTCCCTTTGGTTTTTCATATTTAAA GCAGGGGGGGGCTACAGAAAAGCCCCTTTCTTCCTCTGTTTGCAGGGGAGTGTGGCCCTG TGGCCTGGGTGGAGCAGTCAT---CCTCCCCCTTCCCCGTGCAGGAGCAGGAAATCAGT GCAGAGGCGGTAAAGAAAGACCGACTGGATTTCCACCAGGGCTGGAAAGGTTACTTCAAA ATGAATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCTTTTGTGTTGCAGTACTGC ATGAATGTGGCCAGGCAGAATAATGACAGTGACTGCGGTGCCTTTGTGTTACAGTACTGC **AAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCCAAACTTCGT** CGGCAGATCTACAAGGAGCTGTGTCACTGCAAACTCACTGTGTGAGCCTCGTACCCCAGA CCCCAAGCCCA----TAAATGGGAAGGGAGACATGGGAG----TCCCTTCCCAAGAAACT TGTTTCA----ATTTCTGTATTTTTTTTTTTCTTTGAGAATACTTGTTGATTTCTGATGT BP. 1507 (first entry) 1863 TACGTATATATA 1876 TATATATATATA standard; 18-JUL-2001 RESULT 9
AAD05541/c
ID AAD05541 s AAD05541; 1270 1376 1330 1390 1556 1608 1570 1436 1496 1668 1784 1256 1316 1724 1686 1744 1901 à g ò q ò d οy g ٥y qq ò g δ g δ q ò Бþ δý g δŽ a ò g 

Homo sapiens

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protein genes, and AAE01672-AAE01743 represent the proteins they encode.

protein genes, and AAE01672-AAE01743 represent the proteins they encode.

AAE01744-AAE0163 represent human secreted protein fragments or variants.

The secreted proteins and their genes are useful for preventing.

The secreted proteins and their genes are useful for preventing.

The secreted proteins and their genes are useful for preventing.

The secreted protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the amount of the new genes. Specific uses are described for each of the mount of the new genes. Specific uses are described for each of the and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental aborders, cancer, tumours, foetal and developmental aborders, and include daveloping products for the diagnosis or treatment of aborders, and sacratic disorders (e.g., Alzheimer's disease, Parkinson's diseases), cognitive disorders, disbetes, atherosclerosis, skin disorders, and infections. The proteins can also be used to aid wound the land organs before transplantation, for supporting cell culture of primary tissues, to respendent tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used to a brith-dise sensific for a protein of the honeauxis, and can be used to a brith-dise sensific for the modify storage properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in diagnostic immunoassays e.g., radioimmunoassay or enzyme lin immunosorbent assay (ELISA). The present sequence represents a
                                                                          /product= "Human secreted protein precursor"
                                                                                                             /partial
416.493
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/product= "Mature human secreted protein"
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                                                                                             'note= "Does not include start codon"
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                      ocation/Qualifiers
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27-JUL-2000; 2000US-0221366.
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                    Key
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SQ Sequence 1507 BP; 357 A; 385 C; 354 G; 401 T; 10 other;

Query Match

Best Local Similarity 98.5%; Pred. No. 2e-308;

Matches 1358; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 558 GGTTTGGGGGACAATCTGGGCCAGAAGGGGAGCGCACTTGGCACCCTGATGCCAGCA 617
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qq

1127 ATGGCAGCCTCATACCCCTCAGCACTGAYGAGGTAGTAGAGAARYTRGAGGACATTTTCC 1168 AGCAGGAGTTYTCYACMCCTTCCAGGAAGGGCCTGGTGYTGCAGCTGATCCAGTCKTACC 1108 1158 TGGACATCTTCAATAAGGAGCTACTGCTAATCCCCCATCCACCTGGAGGTGCATTGGTCCC 1217 TGACCATGGATGACTTGGGGACCTTGTATGGACAGAACTGGCTCAATGACCAGGTGATGA 1037 ACATGTATGGAGACCTGGTCATGGACACAGTCCCTGAAAAGGTGCATTTCTTCAATAGTT 1097 TCTTCTATGATAAACTCCGTACCAAGGGTTATGATGGGGTGAAAAGGTGGACCAAAAACG 1157 ATGACAGTGACTGTGGTGTTTTGTGTTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGC 1457 CATTCAGCTTCACCCAGCAGGACATGCCCAAACTTCGTCGGCAGATCTACAAGGAGCTGT 1517 GTCACTGCAAACTCACTGTGTGAGCCTCGTACCCCAGACCCCCAAGCCCCATAAATGGGAAG 1577 GGAGACATGGGAGTCCCTTCCCAAGAAACTCCAGTTCCTTTCCTCTTTGCCTCTTCCCA 1637 208 737 808 388 1407 TCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCCCAGGAGCTTTTTCAGGGCT ACCGCCGCTGCCTAAGCATATTGCCAAGTATCTACAGGCAGAGGCGGTAAAGAAAAACACC 618 TCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCCCAGGAGCTTTTTCAGGGCT CAGATTTGGGCATGGCAGAGAGAGGCAGAGAGGCCTGGGGAGAAAGCCGGCCAGCACAGCC CCCTGCGAGAGGAGCATGTGACCTGCGTACAGAGCATCTTGGACGAATTCCTTCAAACGT CCCTGCGAGAGGAGCATGTGACCTGCGTACAGAGCATCTTGGACGAATTCCTTCAAACGT AGCAGGAGTTTTCCACCCCTTCCAGGAAGGGCCTGGTGTTGCAGCTGATCCAGTCTTACC AGCGGATGCCAGGCAATGCCATGGTGAGGGGCTTCCGAGTGGCTTATAAGCGGCACGTGC ATGGCAGCCTCATACCCCCTCAGCACTGATGAGGTAGTAGAGAAGCTGGAGGACATTTTCC 1287 1167 1107 1038 1098 1218 1338 1398 1458 1518 678 738 798 918 978 687 867 807 687 627 567 507 387 ò qq ò a ö g δý q δ qq δ a ò g δ g ŏ В ò g ò g g ò q 셤 ò 셤 g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The polynucleotide sequences given in AAC59566 to AAC59614 encode the human secreted proteins given in AAB3429 to AAB3437. AAB34348 to AAB34437 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include: neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaccological; and antibacterial. The polynucleotides can be used for the detection of various disorders such as cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The secreted proteins can be used to
                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; and antibacterial; gene therapy; detection; cancer; chromosome marker; chromosome identification; neural disorder; immune disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; profilerative disorder; wound healing; infectious disease; preservative;
                                                 TCTGTTTGCAGGGGAGTGTGGCCCTGTGGCTGGAGCAGTCATCCTCCCCCTTCCC 1817
AGAGAATACTTGTTGATTTCTGATGTGCAGGGGGTGGCTACAGAAAAGCCCCTTTCTTCC 1757
                                                                                                    268
                                                              encoding them, useful for
             Human secreted proteins and gene sequences encoding them, use detecting, preventing, and treating disorders such as cancer, neurological disorders and immune system disorders -
                                                                                                                                                                                                                                                                                                                        Human secreted protein gene 4 SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 340; 429pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Komatsoulis
                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                            AAC59569 standard; cDNA; 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2000; 2000WO-US06822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0126054.
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-587666/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                   food additive; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAB34302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-1999;
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                                                                                                                                                                                                                                                                                               26-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                     AAC59569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ното
1698
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                                                                                                                                                                                                                   RESULT 10
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ID AACS
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1;
                                                                            also be used as a food additive or preservative to increase or decrease storage capabilities. AAC59557 to AAC59565 and AAB34298 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          foctal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; mgiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1766
                                                                                                                                                                                                                                                                                                                                         1347 TCCACCAGGGCTGGAAAGGTTACTTCAAAATGAATGTGGCCAGGCAGAATAATGACAGTG 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1527 AACTCACTGTGTGAGCCTCGTACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGACATG 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wound healing, and infectious diseases. The proteins can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 ACTGTGGTGCTTTTGTGTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCT 129
                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein-encoding gene 11 cDNA clone HOFOB27, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                       10 TCCACCAGGGCTGGAAAGGTTACTTCAAAATGAATGTGGCCAGGCAGAATAATAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 TCACCCAGCAGACATGCCCAAACTTCGTCGGCAGATCTACAAGGAGCTGTGTCACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 AACTCACTGTGTGAGCCTCGTACCCCAGACCCCAAGCCCCATAAATGGGAAGGGAGACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1467 TCACCCAGCAGGACATGCCCAAACTTCGTCGGCAGATCTACAAGGAGCTGTGTCACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1707 TIGTIGATITICIGATGIGCAGGGGGGGGCTACAGAAAAGCCCCTTTCTTCTTCTTGTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGTGGTGCTTTTGTGTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                    650;
                                                                                                                                                                                                                                    21; Length
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                 Sequence 650 BP; 164 A; 155 C; 149 G; 182 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.5%; Score 567.4; DB 21 99.7%; Pred. No. 3.1e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
disorders such as neural, immune,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                Local Simi
hes 579;
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                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                        Matches
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Page 15

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                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMD05492-AAD05564 represent CDNAs corresponding to 22 human secreted protein genes, and AAE01672-AAE01743 represent the proteins they encode. Drotein genes, and AAE01672-AAE01743 represent the protein step encode. CC AAE01743 represent the protein fragments or variants. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing the camount of the new protein in a sample or by determining the presence of muntations in the new genes. Specific uses are described for each of the camount of the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions and infections, for the disorders of the immune system, allorgies, neurological disorders (e.g., rheumatoid arthritis), inflammation, allorgies, neurological disorders (e.g., rheumatoid arthritis), inflammation, allorgies, neurological disorders (e.g., rheumatoid arthritis), inflammation, cardiovascular disorders, programicy schizorders, schizophrenia, asthma, skin disorders, organitive disorders, schizophrenia, asthma, cardiovascular disorders, programicy related disorders, endocrine cardiovascular disorders, programory related disorders, endocrine cardiovascular disorders, programory related disorders, endocrine culture of primary tissues, to regenerate tissues, to identify their cognitive of primary tissues, to regenerate tissues, to identify their cognitive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in companion of the invention endocribed by and intention of the invention of beaution of processervative to modify storage properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.7%; Score 551; DB 22; Length 695; 90.2%; Pred. No. 2.2e-119; Live 5; Mismatches 56; Indels
                                                                                                                                             "Human secreted protein precursor"
                                                                                                                                                                                                                                        /product= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 695 BP; 131 A; 224 C; 217 G; 117 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein-encoding cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olsen HS,
cell culture; chemotaxis; food additive; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 446-447; 540pp; English.
                                                                                        Location/Qualifiers
27..167
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                             01-NOV-2000; 2000WO-US30036.
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27-JUL-2000; 2000US-0221366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soppet DR, Komatsoulis G,
                                                                                                                            /*tag= a
/product=
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159..164
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                                                                                                                                                                                                                                                                        WO200134767-A2
                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                           17-MAY-2001
                                                                                                                                                                sig_peptide
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Human; eukaryotic transcription factor 4A; eIF4Al; promoter;
DNA construct; DNA vaccine; gene therapy; cancer; Parkinson's disease;
cystic fibrosis; hepatitis; HIV; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                     376 GGTGCTCTCATGGCTGAGGATGGGATGAGAGGGTCTCCACCGATGTCCTCTGGGCCCCCA 435
GAAGAGGAGGATGAGGATGAAGATGAGGAAGAGGAAGTGGCAGCTTGGAGGCTGCCCCCC 76
                                                                                                                  436 GTGGAGGAAGATGACGGTGGACTCCAAAGTCTCCTCTGGACCCCTGACTCTGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTGCTCACAGGGGCGGCGGCGAGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAA
                                                                                                                                                                   AGCACCTCGCTGACATTCCACTGGAAGCTTTGGGGGGGCGCCACCGGGGGCCGGCGGGGGG
                                                                                                                                                                                                                                     CTCGCACACCCCAAGAACCATCTTTCACCCCAGCAAGGGGGTGCGACGCCACAGGTGCCA
                                                                                                                                                                                                                                                                                                   TCCCCCTGTTGTCGTTTTTGACTCCCCCCGGGGGCCACCTCCACCCCCGGCTGGGTCTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 CTCTCCTGTACTCTTCCCAATGGCTTTGGGGGACCCCCCGGGCCAGAAGGGGAGCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TGGCACCCCCTGATGCCAGCATCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human eukaryotic initiation factor 4A1 promoter fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             672 GAGAAAGCCGGCCANCACAGCCCC 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716 GAGAAAGCCGGCCAGCACAGCCCC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF55961 standard; DNA; 5318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2000; 2000WO-GB02569.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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14-DEC-1999;
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Gaps

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Best\_Local Similarity 90.2 Matches 617; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                   The present invention describes a DNA construct comprising a transcriptional regulatory sequence linked to the gene of interest wher the regulatory sequence linked to the gene of interest wher the regulatory sequence is the human eukaryotic initiation factor 4A1 (eIF4A1) gene promoter. This can be used in the production of DNA vaccines and gene therapy, both of which can be used in the prevention and treatment of diseases such as cystic fibrosis, parkinson's disease, cancer, hepatitis B and C, HIV, tuberculosis, HPV, HSV, multiple sclerosis, Alzheimer's disease and asthma. It can also be used in
                                                                                                                                                                                                                                                                                                                    1427 CAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCC 1486
                                                                                                                                                                                                                                                                                                                                3827 CAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCTGCAGCAGGACATGCCC 3886
                                                                                                                                                                                                                                                                                                                                                                AAACTTCGTCGGCAGATCTACAAGGAGCTGTGTCACTGCAAACTCACTGTGTGAGCCTCG 1546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGGGTGGCTACAGAAAAGCCCCTTTCTTCCTCTGTTTGCAGGGGAGTGTGGGCCCTGTG 1785
                                                                 New DNA constructs, useful in gene therapy for treating or preventing chronic inflammatory reactions such as multiple sclerosis or asthma, a DNA vaccines, or in the commercial production of proteins
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                           ATGTTTCAATTTC-TGTATTTTTTTTTTTTGAGAGAATACTTGTTGATTTCTGATGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5318;
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                                                                                                                                                                                                                                                  Sequence 5318 BP; 1327 A; 1210 C; 1423 G; 1350 T; 8 other;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                               Score 486.4; DB 22;
Pred. No. 7.6e-104;
                        Ford MJ;
                                                                                                                                                                                                                              vaccines for contraception or drug addiction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4367 AAAAATGCCACGGTCCTGCTCTGGTCAATAAAG 4399
                                                                                                                                                                                                                                                                                              1; Mismatches
                        Catchpole IR,
                                                                                                               Claim 19; Page 58-62; 62pp; English
                                                                                                                                                                                                                                                                        Ouery Match 24.4%;
Best Local Similarity 94.9%;
Matches 544; Conservative 1
                        ú
(GLAX ) GLAXO GROUP LTD
                                            WPI; 2001-138151/14
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AAI94288 standard; cDNA; 870

AAI94288/c

RESULT 13

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The invention relates to novel genes (AA193926-AA197963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy an susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 GACCCTGACTCGGGCCTCCTTTCATGTACTCTGCCCAACGGTTTTGGGGGACAATCTGGG
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                                                   neuroblastoma; malignancy; cancer; tumour marker; N-myc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 870;
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Human neuroblastoma expressed polynucleotide SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 23.5%; Score 468.4; DB 22; Best Local Similarity 94.3%; Pred. No. 5.9e-100; Matches 533; Conservative 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 308-309; 2979pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for N-myc and TrkA genes
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(HISM ) HISAMITSU PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                    07-MAR-2000; 2000JP-0159195.
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                                                                                                                                                           WO200166719-A1.
                                                                                                          Homo sapiens.
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                                                         Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of ovarian cancer. The compositions comprise one or more ovarian tumour the proteins, their associated polynuclectides, or immunogenic portions of the proteins. The ovariant tumour polynucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, and administering to the patient. The sequences can be used as markers for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutuant species and for preparing other genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises compositions used for the therapy and diagnosis
                                                                                                                                                                                                                                                                                                                                               Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss; gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides encoding ovarian tumour proteins, useful for ating ovarian cancer, and as probes, primers, and markers of cancer
                                                         GGACCTTGTATGGACAGAACTGGCTCAATGACCAGGTGATGAACATGTATGGAGACCTGG 1055
CCATGGTGAGGGGCTTCCGAGTGGCTTATAAGCGGCACGTGCTGACCATGGATGACTTGG 995
                 Score 442; DB 22; Length 503;
Pred. No. 7.3e-94;
0; Mismatches 0; Indels 51
                                                                                                                                                                                                                                                                                                                   Human ovarian PCR-subtracted cDNA library clone #1614
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                                                                                                                     1056 TCATGGACACAGTCCCTGAAAAGGT 1080
                                                                                                                                    331 TCATGGACACAGTCCCTGAAAAGGT 307
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ilarity 90.8%;
Conservative
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28-MAR-2000; 2000US-0192745.
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                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                            AAS25529 standard;
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                                                                                                                                                                                                                                                                                                                                                                                primer; probe.
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                                                                                                      1351 CCAGGGCTGGAAAGGTTACTTCAAAATGAATGTGGCCAGGCAGAATAATGACAGTGACTG 1410
                                                                                                                                                                                                             1411 TGGTGCTTTTGTGTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCAC 1470
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TGTGAGGCGACGCACCATCACCTATTTTGACTCGCAGCGTACCCTAAACCGCCGCTGCCC
                                                                                                                                                                                                                                                                 1471 CCAGCAGGACATGCCCAAACTTCGTCGGCAGATCTACAAGGAGCTGTGACTGCAAACT
                                                                                                                                                                                                                                                                                 194 CCAGCAGGACATGCCCAAACTTCGTCGCGCAGATCTACAAGGAGCTGTGTGTCACAAACT
                                                                                                                                                                                                                                                                                                                                     Human neuroblastoma expressed polynucleotide SEQ ID NO 33.
                                                                                                                                                                          263 CCAGGGCTGGAAAGGTTACTTCAAAAT-----------
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                              The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  996 GGACCTIGIAIGGACAGAACIGGCICAAIGACCAGGIGAIGAACAIGIAIGGAGACCIGG 1055
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                                                                                                                                                                                                                                               517 TGGACCCTGACTCGGGCCTCCTTTCATGTACTCTGCCCAACGGTTTTGGGGGGACAATCTG 576
                                                                                                                                                                                                                                                                  577 GCCCAGAAGGGGAGCGCACTTGGCACCCCCTGATGCCAGCATCCTCATCAGCAATGTGTG 636
                                                                                                                                                                                                                                                                                                                                CAGCATCGGGGACCATGTGGCCCCAGGAGCTTTTTCAGGGCTCAGATTTGGGCAGA 696
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                                                                                                                                                                                                                    14;
                                                                                                                                                                                DB 22; Length 820;
                                                                                                                                                                                Score 362.2; DB 22; Length
Pred. No. 4.7e-75;
0; Mismatches 70; Indels
                                                                                                                                               Sequence 820 BP; 224 A; 223 C; 170 G; 191 T; 12 other;
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Claim 1; Page 59; 2979pp; Japanese
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Best Local Similarity 85.1%;
Matches 481; Conservative
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Search completed: December 16, 2002, 15:38:59 Job time : 418 secs

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                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Williamson, Valerie M.
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yadhoobi, Jafar
APPLICANT: Tadhoobi, Jafar
APPLICANT: Milligan, Stephen
APPLICANT: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/947,823

FILING DATE: 09-0CT-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/18802

FILING DATE: 09-0CT-1997

PRIOR APPLICATION NUMBER: US 60/028,191

FILING DATE: 09-0CT-1997

APPLICATION NUMBER: US 60/028,191

FILING DATE: 10-0CT-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
              US-07-799-828C-8
US-08-074-275-8
US-08-074-275-8
US-08-191-211-3
US-09-191-211-3
US-08-207-904-18
US-09-207-904-18
US-09-207-904-18
US-09-791-71-79
US-09-791-71-79
US-09-791-79
US-09-791-79
US-09-724-394A-21
US-08-724-394A-21
US-09-724-394A-21
US-09-727-217-55
US-09-604-838-89
US-09-604-838-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08947823
Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 51952 base pairs;
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-947-823-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
128
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87350
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15062
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   US-08-947-823-1
   000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Appli
Patent No. 5312912
Sequence 4, Appli
Sequence 1, Appli
Sequence 17, Appli
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atent No. 5312912
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Sequence 4, Appli
                                                                                                                                             (without alignments)
9540.522 Million cell updates/sec
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1991
1 GCTCCCTGTCCCCGACCC.....TGCTCTGGTCATAAAGATC 1991
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                                                                                                                         December 16, 2002, 13:18:49; Search time 64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-616-368A-17
US-09-054-298-17
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-08-616-368A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-922-723A-8
US-07-799-828C-8
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-08-818-655-17
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US-08-577-483-7
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-08-480-366-8
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US-08-550-544-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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67.2
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PCT/US97/18802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-947-823-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18872
REFERENCE/DOCKET NUMBER: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                 LENGTH: 51952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 90.0%
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                 FILING DATE: 09-OCT-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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US-08-282-581-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: 199700101
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                 Length 51952;
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES; FOR GENETICALLY ENGINEERING DISEASE RESISTANCE AND OTHER INDUCIBLE TRAITS IN PLANTS; NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
FILING DATE: 13-JUN-1989
                                                       20; Indels
                                                                                                                                                                                           Db 13725 ATATATATATATATATATATATTATTCTTATAAAAAAA 13766
                                                                                                                                                                                                                                                                                   5312912-3
;Patent No. 5312912
; APPLICANT: HADWIGER, LEE A.;CHIANG, CHIN C.;HOROVITZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1919 TATATATATATATATATATATATATATATAAATATATAAAT 1961
                                                                                                                                                                     1948 ATAAATATAAATGCCACGGTCCTGCTCTGGTCAATAAAGA 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NOTA:
ELLING DATE: 09-OCT-1997
               Score 70; DB 3; I
Pred. No. 6.6e-08;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yaghoobi, Jafar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-947-823-1/c
; Sequence 1, Application US/08947823
; Patent No. 6114605
               3.5%;
                                                     Conservative
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                                 1 Similarity
82; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1890
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               Query Match
Best Local S
Matches 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Cramer, Carole L.

APPLICANT: Cramer, Deborah L.

APPLICANT: Weissenborn, Deborah L.

TITLE OF INVENTION: HMG2 PROMOTER EXPRESSION SYSTEM AND

TITLE OF INVENTION: POST-HARVEST PRODUCTION OF GENE PRODUCTS

TITLE OF INVENTION: IN PLANTS AND PLANT CELL CULTURES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWA APPLICATION DATA:
APPLICATION NUMBER: US/08/282,581
FILING DATE: 29-JUL-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                   FILING DATE: 10-CCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELEFONMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1155 Avenue of the Americas
US 60/028,191
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LENGTH: 1890
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   LOCATION:
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US-08-282-581-4
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                                                                                                LOCATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5312912-3
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                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                             Length 480;
                                                                                      LOCATION: 162
OTHER INFORMATION: /label= n
OTHER INFORMATION: /note= "n=x=Unknown nucleotide"
                                                                                                                                                                                          ): OTHER INFORMATION: /label= n
): OTHER INFORMATION: /note= "n=x=Unknown nucleotide"
US-08-282-581-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cramer, Carole L.
APPLICANT: Weissenborn, Deborah L.
TITLE OF INVENTION: HMG2 PROMOTER EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      1952 ATATATAAATGCCACGGTCCTGCTCTGGTCAATAAAGAT 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATATATATATATGCAGAGTATCTTTGTAGATTATAAT 207
                                                                                                                                                                                                                                                                         3.4%; Score 67; DB 1; 79.8%; Pred. No. 3.9e-08; Live 0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,816
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7956-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/550,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08550544
Patent No. 5689056
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18872
REFERENCE/DOCKET NUMBER: 79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                NAME/KEY: modified_base
                                                                       NAME/KEY: modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 480 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                         Query Match 3.4°
Best Local Similarity 79.8
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-550-544-4/C
                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
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Patent No. 5670349
GENERAL INFORMATION:
APPLICANT: Cramer, Carole L.
APPLICANT: Weissenborn, Deborah L.
APPLICANT: Weissenborn, Deborah L.
TITLE OF INVENTION: HOG2 PROMOTER EXPRESSION SYSTEM AND
TITLE OF INVENTION: POST-HARVEST PRODUCTION OF GENE PRODUCTS
WINDOW OF GENERAL OF THE PRODUCT OF THE PROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES; FOR GENETICALLY ENGINEERING DISEASE RESISTANCE AND OTHER INDUCTBLE TRAITS IN PLANTS; NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
PILING DATE: 13-JUN-1989
                                                                                                                                                                                                                                                                                                                                                               Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Indels
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                                      /note= "n=x=Unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
5312912-3/c
;Patent No. 5312912
; APPLICANT: HADWIGER, LEE A.;CHIANG, CHIN C.;HOROVITZ,
                                                                                                                                                                                                      /label= n
/note= "n=x=Unknown nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 ATATATATATATAACAACTCAATATCTCTGTCATAATTAT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1952 ATATATAAATGCCACGGTCCTGCTCTGGTCAATAAAGAT 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 ATATATATATATGCAGAAGTATCTTTGTAGATTATAAT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 66.2; DB 6; 77.7%; Pred. No. 1.2e-07; tive 0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 1;
Pred. No. 3.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: FENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
OTHER INFORMATION: /label= n
OTHER INFORMATION: /note= "n=
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                   3.4%;
                                                                                                                  modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   79; Conservative
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COTHER INFORMATION:
US-08-550-544-4
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Best Local Similarity
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Best Local Similarity
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TITUY: New York
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Query Match 3.3%; Score 65.8; DB 1; Length 480; Best Local Similarity 90.9%; Pred. No. 8e-08; Matches 70; Conservative 0; Mismatches 7; Indels
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Patent No. 5767262
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Haber, Edgar
APPLICANT: Haber, Edgar
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
CORRESPONDENCE: 1518 & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /label= n
OTHER INFORMATION: /note= "n=x=Unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= n
/note= "n=x=Unknown nucleotide'
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ZIP: 0210-2804
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER: 05433/022001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-1996
                                                                               7956-004
              ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18872
REFERENCE/DOCKET NUMBER: 7956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1944 ATATATAATATATAAA 1960
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286 ATATATATATATATA 302
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fraser, Janis K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 15
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 225 F1
CITY: Boston
STATE: MA
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US-08-616-368A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified_base
Location: 162
OTHER INFORMATION: /label= n
OTHER INFORMATION: /note= "n-x-Unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 356

; O'THER INFORMATION: /label= n

O'THER INFORMATION: /note= "n=x=Unknown nucleotide"

US-08-282-581-4
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APPLICANT: Weissenborn, Deborah L.
TITLE OF INVENTION: HMG2 PROMOTER EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,581
FILING DATE: 29-JUL-1994
CLASSIFICATION: 800
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/550,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,816
PC-DOS/MS-DOS
                                                                      FILING DATE: 29-JUL-1994
CLASSIFICATION: 800
ATTORNEYAGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18872
REFERENCE/DOCKET NUMBER: 7956
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-90-9090
TELESAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5-08-550-544-4
Sequence 4, Application US/08550544
Patent No. 5689056
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1944 ATATATAAATATAAAA 1960
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Best Local Similarity 90.99
Matches 70; Conservative
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CLASSIFICATION: 800
OPERATING SYSTEM:
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            9; Indels
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                                                                                                                                                                                                                                 APPLICANT: Lee, Mu-En

APPLICANT: Haber, Edgar
APPLICANT: Haber, Edgar
TITLE OF INVENTION: SWOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 46
CORRESPONDER ADDRESS:
ADDRESSEE: Fish & Richardson " C
STREET: 225 Frant'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows95
SOFTWARE: Fast5ED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,655
FILING DATE: 14-MAR-1997
CLASSIFICATION 1514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY,AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                               Sequence 17, Application US/08818655 Patent No. 6258557
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US-09-433-579-3/c
; Sequence 3, Application US/09433579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 297 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71; Conservative
          71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 02110-2804
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                 US-08-818-655-17
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            Matches
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                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                          Score 65.6; DB 1; Length 297;
Pred. No. 7.1e-08;
0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OCHEVIER: 150 COMPOLIANTE
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY-AGENT INFORMATION:
NAME: Beattie, Ph.D., Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 05433/022002
TELEPHONE: 611/542-5070
TELEPHONE: 611/542-8006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,3%; Score 65.6; DB 3;
88.8%; Pred. No. 7.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09054298 Patent No. 6136953
                                                                                                                                                                                                                                                                                                                                                    1940 ATATATATATATATA 1959
                                                                                                                                                                                                                                                                                                                                                                      17:
                                                                                                                                                                                                               3.3%;
88.8%;
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 297 base pairs TYPE: nucleic acid STRANDEDNESS: both LOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Diskette
IBM Compatible
       : 617/542-5070
617/542-8906
                                                                                                                                                                                                    Ouery Match
Best Local Similarity 88.89
Watches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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FDNESS: both
                                                                                                                                                             MOLECULE TYPE: DNA
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Best Local Similarity
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STRANDEDNESS:
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                                                                                                                                                                             US-08-616-368A-17
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Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08074275
Patent No. 5468610
GENERAL INFORMATION:
APPLICANT: Drs. Carl R. Merril and
APPLICANT: Minael H. Polymeropoulos
TITLE OF INVENTION: THREE HIGHLY INFORMATIVE REPEAT
TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.2%; Score 64.6; DB 1;
80.0%; Pred. No. 8.6e-08;
tive 0; Mismatches 19;
                                                                        1931 TATATATATATATATATATAAATATAAATGCCA 1965
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                                                                                           STATE: Virginia
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/799,828C
FILING DATE: 19911127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   Sequence 8, Application US/07799828C Patent No. 5378602 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 71708
TELECOMMUNICATION INFORMATION:
TELECHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-07-799-828C-8
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Best Local Similarity
Matches 76; Conserv
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US-07-799-828C-8/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Drs. Mihael H. Polymeropoulos
APPLICANT: and Carl R. Merril
TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE
TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.2%; Score 64.6; DB 1;
80.0%; Pred. No. 8.6e-08;
tive 0; Mismatches 19;
                                                                                                                                                                                                                                                                         Score 65; DB 4; Pred. No. 7.8e-07; 0; Mismatches 15
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             GENERAL INFORMATION:
APPLICANT: Rottmann, William H.
TITLE OF INVENTION: LSAG Gene
CURRENT APPLICATION NUMBER: US/09/433,579
CURRENT APPLICATION NUMBER: US/09/433,579
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 17656
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CURRENT APPLICATION. DATA:
APPLICATION NUMBER: US/07/922,723A
FILING DATE:
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REGISTRATION NUMBER: 34506
REFERENCE/DOCKET NUMBER: 717081B
TELEPHONICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/07922723A Patent No. 5369004 GENERAL INFORMATION:
                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Liquidambar styraciflua
US-09-433-579-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic) US-07-922-723A-8
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Best Local Similarity 83.1%;
Matches 74; Conservative
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Best Local Similarity 80.0°
Matches 76; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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December 16, 2002, 14:16:54; Search time 133 Seconds (without alignments) 5920.021 Million cell updates/sec
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1991
1 GCTCCCTGTCCCCCGACCC......TGCTCTGGTCANTAAAGATC 1991
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1: /cgn2_6/ptodata/1/pubpna/US07_pUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NME_DUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US00_USW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_USW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_USW_PUB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5: 7: 7: 10: 11: 12: 14:

## SUMMARIES

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Result	ult		Query				
	No.	Score	Match	Match Length DB	BB:	OI	Description
	-	1991	100.0	1991	10	US-09-848-852A-4	Sequence 4, Appli
ပ	7	442	22.2	503	10	US-09-777-564-1710	Sequence 1710, Ap
υ	m	368	18.5	432	10	US-09-983-965-835	
	4	92	4.6	435	10	US-09-867-701-4735	Sequence 4735, Ap
υ	S	84.8	4.3	106	10	US-09-867-701-4719	4
υ	9	72.6	3.6	217	10	US-09-969-373-1226	Sequence 1226, Ap
	7	70.8	3.6	217	10	US-09-969-373-1226	П
υ	8	70.6	3,5	138	10	US-09-969-373-792	-
	6	70.6	3.5	169	10	US-09-969-373-741	1-
	10	9.02	3.5	170	10	US-09-969-373-780	780,
	11	9.07	3.5	242	10	US-09-969-373-781	-
	12	70.4	3.5	123	10	US-09-969-373-182	182,
υ	13	70.4	3.5	202	10	US-09-969-373-5	Sequence 5, Appli
	14	70.4	3.5	229	10	US-09-969-373-1068	Sequence 1068, Ap
ບ	15	70	3.5	170	10	US-09-969-373-82	
	16	70	3.5	209	10	US-09-969-373-1107	
O	17	69.4	3.5	144	10	US-09-969-373-38	Sequence 38, Appl
	18	69.4	3.5	741	10	US-09-910-943-479	Sequence 479, App
	19	69.2	3.5	212	10	US-09-969-373-1097	Sequence 1097, Ap

ATTORREY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0515 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1991 base pairs
TYPE: nucleic acid

APP APP APP APP APP APP APP APP APP APP	
2337, 1517, 13181, 1463, 1463, 1616, 1616, 170, 170, 170, 170, 170, 170, 170, 170	
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373 - 237 373 - 1517 373 - 1613 373 - 1013 373 - 1463 373 - 1463 373 - 1652 373 - 1652 373 - 1652 373 - 1653 373 - 173 373 - 174 373 - 174 374 - 174 375 - 174 37	TATED WITH rals, Inc.  Version 2  Wersion 2
US-09-966-373 US-09-966-373 US-09-966-373 US-09-966-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373 US-09-969-373	IGNMEN L. ASSOCI adows ndows 9/848,
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41122221222122222222222222222222222222	cation US/0984, 1006373A1 Tang, Y. Tom Corley, Y. Tom Corley, Neil Guegler, Karl Yuw Henry NewTION: Patterson, Ch. Wenrion: Patterson, Ch. Ca. Ca. Ca. Ca. Ca. Ca. Ca. Ca. Ca. Ca
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                                                                                                                                                                                                                                                                                                                                                                                                                            ACCCCCTGATGCCAGCATCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCCCA
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                                                                Length
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                                                              100.0%; Score 1991;
100.0%; Pred. No. 0;
ive 0; Mismatches
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                                      SEQUENCE DESCRIPTION: SEQ
STRANDEDNESS: single
                      LIBRARY: BEPINOT01
CLONE: 2056178
       TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                              Conservative
                                                               Query Match
Best Local Similarity
Matches 1991; Conserv
                                              .09-848-852A-4
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCELE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 835
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Fatent No. US2002013237A1

GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 432;
                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: 29-LIB188-017-Q1-E1-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                     18.5%; Score 368; DB 10; 91.7%; Pred. No. 3.1e-84; tive 0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 503;
                                                                                                                                                                                                                         FOR THE THERAPY CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 442; DB 10;
Pred. No. 4.7e-103;
0; Mismatches 0;
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                                                                                                                               Sequence 1710, Application US/09777564
Fatent No. US200202591A1
GENERAL INFORMATION:
APPLICANT: AJGATE, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CAN; FILE REPERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER: OF SEQ ID NOS: 1730
SOFTWARE: FastSEQ for Window Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-983-965-835/c
Sequence 835, Application US/09983965;
Patent No. US20020137160A1
GENERAL INFORMATION:
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1 Similarity 90.8%;
503; Conservative
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; ORGANISM: Homo sapiens
US-09-777-564-1710
                                                 1981 CAATAAAGATC 1991
                                                                                                   RESULT 2
US-09-777-564-1710/c
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SEQ ID NO 1710
LENGTH: 503
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; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1226
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US-09-969-373-792/c
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US-09-969-373-1226
 LENGTH: 217
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Petent No. US20020133852A1

GENERAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Effertz, Roger J.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REPERENCE: 38-10(52679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-10-02

PRIOR PILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 09/754,853

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR PILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 4593
                                                                                                         Query Match 4.6%; Score 92; DB 10; Length 435; Best Local Similarity 100.0%; Pred. No. 6.1e-14; Matches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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Pred. No. 1.8e-12;
0; Mismatches 2;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4735
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Best Local Similarity 97.7%;
Matches 86; Conservative
                                              TYPE: DNA
ORGANISM: Homo sapien
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CORGANISM: HOMO sapien
US-09-867-701-4719
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US-09-867-701-4719/c
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US-09-969-373-1226/c
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LENGTH: 106
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    Length 217;
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Pred. No. 1e-08;
0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                         Sequence 1226, Application US/09969373
; Sequence 1226, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Effertz, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REPERBUES: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 4593
; TEMPOR 1226
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; Sequence 792, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
                                           Indels
                                                                                                                                                                         Score 72.6; DB 10;
Pred. No. 3.5e-09;
0; Mismatches 19;
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Best Local Similarity 91.5%;
Matches 75; Conservative (
    Query Match 3.6%;
Best Local Similarity 81.6%;
Matches 84; Conservative
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NUMBER OF SEQ ID NOS: 4593
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US-09-969-373-781
                                                                                         US-09-969-373-780
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                                    LENGTH: 170
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LENGTH: 242
                     SEQ ID NO 780
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                                                                                                                             Query Match
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GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION:
FILE REFERENCE: 38-10(52679)A;
CURRENT APPLICATION NUMBER: US /09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
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Patent No. US20020133852A1

GENERAL INFORMATION:

APPLICANT: Effertz. Roger J.

APPLICANT: Hauge, Brian M.

TITLE OF INVENTION: SOPPEAN SSRs and Methods of Genotyping
FILE REPERENCE: 38-10(52679)A

CURRENT FILING DATE: 2001-10-02

PRIOR FILIGE DATE: 2001-01-05

PRIOR FILIGE DATE: 2001-01-05

PRIOR FILIGE DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR FILING DATE: 2001-01-01-3

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13
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84.9%; Pred. No. 9.8e-09;
                                                                                                       Score 70.6; DB 10;
Pred. No. 8.6e-09;
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                                                                                                      3.5%;
78.0%;
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                                  ; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-792
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; ORGANISM: Glycine max
US-09-969-373-741
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US-09-969-373-780
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US-09-969-373-741
SEQ ID NO 792
LENGTH: 138
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LENGTH: 169
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                                                                                                 3.5%; Score 70.6; DB 10; Length 170; 81.2%; Pred. No. 9.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 781, Application US/09969373
Fatent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Effertz. Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR PRILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
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APPLICANT: Efferts, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT APPLICATION NUMBER: US 09/754,853
PRIOR PRILING DATE: 2001-01-05
PRIOR PLILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR PLING DATE: 2001-01-13
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                                                                                                                                                    82; Conservative
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TYPE: DNA ORGANISM: Glycine max
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Matches 82; Conserv
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PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 1068
LENGTH: 229
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                                                                                                                                 Length 123;
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Patent No. US20020133852A1

GENERAL INPORMATION:

APPLICANT: Effertz. Roger J.

APPLICANT: Effertz. Roger J.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38010(52679)A

CURRENT FILIG DATE: 2001-10-02

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

SEQ ID NOS: 4593

SEQ ID NOS: 4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 202;
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; Sequence 1068, Application US/09969373
; GENERAL INCORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679) A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                  21; Indels
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Pred. No. 9.1e-09;
0; Mismatches 21;
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83.3%; Pred. No. 1.2e-08;
tive 0; Mismatches 16;
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ilarity 79.8%;
Conservative
 PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 182
LENGTH: 123
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Matches 83; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-5
                                                                                 ; ORGANISM: Glycine max US-09-969-373-182
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US-09-969-373-5/c
                                                                    TYPE: DNA
                                                                                                                                   Query Match
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                                                                                Length 229;
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| Patent No. US2002013385241
| GRNERAL INFORMATION:
| APPLICANT: Effertz.
| APPLICANT: Effertz.
| APPLICANT: Effertz.
| APPLICANT: Effertz.
| APPLICANT: Bayes. Brian M.
| TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping FILE REFERENCE: 38-10(52679)A.
| CURRENT APPLICATION NUMBER: US/09/969,373
| CURRENT FILING DATE: 2001-10-02
| PRIOR APPLICATION NUMBER: US 09/754,853
| PRIOR APPLICATION NUMBER: US 09/760,427
| PRIOR PILING DATE: 2001-01-13
| PRIOR FILING DATE: 2001-01-13
| PRIOR FILING DATE: 2001-01-13
| PRIOR FILING DATE: 2001-05-15
| NUMBER OF SEQ ID NOS: 4593
| SEQ ID NO 82.
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                                                                              Score 70.4; DB 10;
Pred. No. 1.3e-08;
0; Mismatches 16;
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                                                                                                                                                                                                                                                  1926 ATATATATATATATATATATATATATATATATATA 1961
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                                                                                Query Match 3.5%;
Best Local Similarity 83.3%;
Matches 80; Conservative
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1068
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; ORGANISM: Glycine max
US-09-969-373-82
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Title: Perfect score: Sequence:

Run on:

Scoring table:

Searched:

Database :

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 1071)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gappa-remail.nih.gov

Tissue Procurement: ATCC/COTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM12258 row: 1 column: 15

High quality sequence stop: 648.

rce 1..1071
                                     BQ43358 AGENOURT
BQ433549 G03367640
ALS79669 ALS79669
AW961869 EST373942
BG870520 G02791439
BM69661 UI-E-DW0-
BI456217 G03172996
BI079603 G02876423
ALS78220 ALS78220
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BQ186996 UT-E-EJI-
BR164921 G0178153
BC001101 UT-H-DHI-
AW08552 Wy67b03.x
BI732013 603355881
AV721960 AV721960
AW578424 RCI-CT024
AW604359 RCI-CT024
AW64359 RCI-CT024
AW64359 RCI-CT024
AW94755 EST376963
AZ399027 IMO164LIO
AI800802 Wg13d04.x
BE668566 MXI_00144
BW916790 EST348198
BI247525 602960160
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AGENCOURT_6542888 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548958
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BQ220291 AGENCOURT
BM507574 ih41e03.y
BF139554 601785671
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BF195133 7n15f03.x
BM670002 UI-E-DX1-
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BQ021355 UI-H-DH1-
BG865703 602783877
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                            BQ057204
BQ433698
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673.8
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1 GCCICCCTGICCCCCGACCC......TGCICTGGICAATAAAGAIC 1991
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             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Score

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PM3-ET027 AGENCOURT

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// Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InAGE:5554637"
/clone=!up="lymphoma, cell line"
/lab_host="DH10B (phage-resistant):
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
326 c 311 g 236 t
                                                                                                                                                                                                                                                                                              bp mRNA linear EST 05-MAR-2002
Homo sapiens cDNA clone IMAGE:5554637
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1134)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1134)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can little Afficiation of the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM12273 row: i column: 06
                                                                                                     286 GGCGGCGGGGCCTCGCACACCCCAAGAACCATCTTTCACCCCAGCAAGGGGGGTGCGACGC
      1581 GACATGGGAGTCCCTTCCCAAGAAACTCCAGTT-CCTTTCCTCTTTGCCTCTTCCTACCACT
                                                                                CACAGGTGCCATCCCCCTGTTGTCGTTTTGACTCCCCCGGGGGCCCACCTCCACCCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.8%; Score 812.2; DB 14; Length 1134; 96.1%; Pred. No. 1.4e-142; ive 0; Mismatches 33; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583.
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AGENCOURT_6492923 NIH_MGC_85
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Location/Qualifiers
1. 1134
                                                                                                                                                           1695 TTGAGAGAATACTTGTTGATT 1715
                                                                                                                                                                                                  980
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BM804530
BM804530.1 GI:19121353
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/organism="Homo sapiens"
/db_xref="taxon:5606"
/clone="laxon:5548958"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
mechanlogies
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&
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Pred. No. 3.5e-154;
0; Mismatches 26;
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Homo sapiens cDNA clone IMAGE:5548865
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NIH-WGC http://mgc.noi.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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AGENCOURT_6542932 NIH_MGC_72 HC
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/db_xref="taxon:9606"
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/lab_not=="Organ: skin; Vector: pCNV-SPORT6; Site_1: Not1;
/note="Organ: skin; Vector: pCNV-SPORT6; Site_1: Not1;
/organ: 
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Email: fliang@ilfetech.com URL:
http://fulllength.invitrogen.com"

17 a 199 c 206 g 190 t 5 others
                                                                                                                                                                                                                         ALSELOW TI_NFLOOR_TC2 Homo sapiens cDNA clone CSODJ013YK06 3 prime, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1282 CCGCTGCCCTAAGCATATTGCCAAGTATCTACAGGCAGA--GGCGGTAAAGAAAGACCGA 1339
                                                               1340 CTGGATTT----CCACCAGGCTGGAAAGGTTACTTCAAAATGAATG--TGGCCAGGCAG 1393
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                                                                                 758 GGTGAAAAGGTGGACCAAAAACGTGGACATCTTCAATAAGGAGCTACTGCTAATCCCCAT 699
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                 Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Onpublished (2001)
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AGENCOURT_6481545 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555330 BM476787
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1114)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can left at:
Clone distribution: MGC clone distribution information can left.//image.llnl.gov
http://image.llnl.gov
Plate: LLAM12275 row: f column: 03
High quality sequence stop: 554.

I. 1114
                                                                                                                                                                        278 CITICCTCTCTTGCTCTTCCCACTTCCCTTTGTTTTTCATTTAAATGTTTCA
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AGENCOURT_7827074 NIH_MGC_67 bp mRNA linear EST 24-WAY-2002 57, mRNA sequence.
BQ440555.
EST. GI:21179631
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I (bases 1 to 867)

I (bases 1 to 867)

INH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

LOntact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LiAM13491 row: o column: 20

High quality sequence stop: 645.
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Catarrhini; Hominidae; Homo.
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/lab_host="retinoblastoma"
/lab_host="setinoblastoma"
/lab_h
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Pred. No. 4.5e-128;
0; Mismatches 10;
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/clone="IMAGE:5555330"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
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No. 1.1e-130;
Smatches 22; Indels 8;
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96.6%;
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/db_xref="taxon:9606"
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AGENCOURT_6545546 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737188
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1099)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lateriate through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12746 row. o column: 13
High quality sequence stop: 663.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
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Score 720.4; DB 13;
Pred. No. 2.4e-125;
0; Mismatches 11;
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NotI; Site_2: SalI; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5.TCGACCCACGCGCCCC3' and
5.TCGACCACGCGCGCCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
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                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. o column: 14
High quality sequence stop: 614.
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 National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 29; Indels
                                                                                                                                                                                                                                                    /organism="Homo sapiens"
//dLxref=taxon:9006"
//clone=IMAGE:6181093"
//clone_lib="Lupski_dorsal_root_ganglion"
                                                                                                                                                                                                                                                                                                                                      /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 994)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gappa-remail.inh.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2062 row: m column: 08

High quality sequence stop: 620.

I. 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENCOURT_6769328 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5812399 5', mRNA sequence. BQ057204.1 GI:19816544 EST.
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                                                                                     CAAACTICGICGGCAGAICIACAAGGAGCIGIGICACIGCAAACICACIGIGIGAGCCIC 1545
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/db_xref="taxon:9606"
/clone="InAGE:5812399"
/tlosue_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B" (phage-resistant)"
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Pred. No. 1.3e-117;
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Homo sapiens cDNA clone IMAGE:6025493
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1 (bases 1 to 936)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                CCAGGGCTGGAAAGGTTACTTCAAAATGAATGTGGCCAGGCAGAATAATGACAGTGACTG
                                                                                                                                 TGGTGCTTTTGTGTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCAC
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18;
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    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can http://image.lln.gov
Plate: LLAM13237 row: 1 column: 06
                                                                                                                                                                                                                                                                                   GGAGTCAGCTGGGAACCTCCCAGCGGCCCCGCCCTTCCCGCCCCACTCATCGAAAAACCT
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Tissue Procurement: ATCC
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/organism="Homo sapiens"
/do_xerf="texon:9606"
/clone_lib="NIH_MGC_91"
/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
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/note="Organ: prostate, Vector: pcWV-SPORT6; Site_1: NotI;
/note="Organ: prostate, Vector: pcWV-SPORT6; Site_1: NotI;
/note="Organ: prostate, Vector: pcWY-SPORT6; Site_1: NotI;
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/note="Organ: prostate, Vector: pcMY-SPORT6; Site_1: NotI;
/note="Organ: pcmy-sport6"/ pcmy-sp
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Catarrhini; Hominidae; Homo.
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                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoo Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 715)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
659 CAGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCAGAAGAGGCCAGAGAGGCCT-GGGGA
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Pred. No. 1.4e-116;
0; Mismatches 12;
                                                                                                                                 718 GAAAGCCGGCCAGCACACCCCTGCGAGAGGAGCA 753
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Plate: LLAM10302 row: o column: 09
High quality sequence stop: 710.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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98.0%;
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/db_xref="taxon:9606"
/clone="csobpulo7yF21"
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/tissue_type="T cells from T cell leukemia"
/tissue_type="T cells from T cell leukemia"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-stranded cDNA was digested with Not I and cloned
into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
Library was constructed by Life Technologies. Contact:
Feng Liang Life Technologies, a division of Invitrogen
9800 Medical Center Drive Rockville, Maryland 20850, USA
Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
87 a 158 c 162 g 147 t 28 others
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                                                                                      1493
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 662
                                                                                                                                                                                                                                        31.9%; Score 634.2; DB 9; Length 662;
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Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 676)
1 (bases 2 to 676)
1 (bases) 1 (bases
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Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                  11;
ed. No. 3.9e-109;
Mismatches 11;
 Pred.
               23;
94.98;
                 Conservative
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BG870520 804 bp mRNA linear EST 29-MAY-2001 602791439F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4922696 5', mRNA sequence.
BG870520
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                                                                                                                              MAGG"
                                                                     Location/Qualifiers
1. 676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE resequences, MAGE a 191 c 212 g 138 t
                                                                                                                                                                                               Score 629.4; DB 10
Pred. No. 3.1e-108;
0; Mismatches 11;
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 167
                                                                                                                                                                                                 31.6%;
98.1%;
                                                         Seq primer: Reverse
                                                                                                                                                                                              Query Match
Best Local Similarity 98.1*
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Email: msoares@blue.weeg.uiowa.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics (www.resgen.com).
Seq primer: M13 Reverse.
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BM696661.1 GI:19009919
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/Clone=lib="NCI_CGAP_SG2"
/Clone=lib="NCI_CGAP_SG2"
/Clone=lib="NCI_CGAP_SG2"
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Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                             E I (bases 1 to 804)

S NHH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Oppublished (1999)

Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov.
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lnl.gov n. column: 09
High quality sequence stop: 789.

Location/Qualifiers
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 804)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="FVB/N"
 BG870520.1 GI:14221060
                                                          Mus musculus
                                       house mouse
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/de_stage="adult"
/lab_host="DH108 (Life Technologies) (Tl phage-resistant)"
/lab_host="DH108 (Life Technologies) (Tl phage-resistant)"
/note="Organ: eye; Vector: pT/T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT-E-DW0 is a cDNA library containing the following
tissue(s): lens. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996 First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT/T3-Pac vector. The
oligonaclectide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 28-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 626)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                             1418 TTTGTGTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAG 1477
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451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                             TGGAAAGGTTACTTCAAAATGAATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCT 1417
                                                                                                                                                                                                                                                                                                                                           692
BM696661 626 bp mRNA linear EST 28-
UI-E-DW0-agk-m-22-0-UI.rl UI-E-DW0 Homo sapiens cDNA clone
UI-E-DW0-agk-m-22-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1538 -TGAGCCTCGTACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGA 1582
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Program for Rat Gene Discovery and Mapping
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/db_xref="taxon:9606"
/clone="UI-E-DW0-agk-m-22-0-UI"
/clone_lib="UI-E-DW0"
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0
sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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